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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Sep 17 16:49:37 1998; MasPar time 10.98 Seconds
425.709 Million cell updates/sec
Tabular output not generated.

#i+10. / YTC-00-7/1-/27-1

Title: ' >US-08-741-437-1
Description: (1-289) from US08741437.pep
Perfect Score: 2134

Perfect Score: 2134
Sequence: 1 MSGFSTEERAAPFSLEYRVF.....CESACTVPTDVDKWFHHQKN 289

Scoring table: PAM 150

hed: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29

Statistics: Mean 33.562; Variance 136.718; scale 0.245

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16 87 17 87	15 88 87	75 CT			13 87		11 89	10 90	9 90	8 91	7 91	6 91	5 91	4 95	3 97	2 100	1 185	Result No. Score
4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.2	4.2	4.2	4.3	4.3	4.3	4.3	4.5	4.5	4.7	8.7	Query Match Length
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W18039	R69731	R28411	R12466	P70155	P70590	R92524	W38272	W38275	P80911	R55198	R60101	R12465	R42424	R42426	P83149	R55200	R98153	Ħ
Human brain 61 kDa Ca	_	Protein encoded by cD	HLA-C exon Cb-2.	Sequence encoded by g	Sequence of the human	Pyrodictium occultum	Bovine parathyroid ce	Rat kidney cell calci	Consensus sequence of	Canine zona pellucida	Canine zona pellucida	HLA-C exon Cb-1.	Rat gustducin alpha s	Bovine rod transducin	Probe F10-encoded pro	Feline zona pellucida	Thermostable inorgani	Description
5.28e+01	5.28e+01	5.28e+01	4.47e+01	5.28e+01	5.28e+01	4.47e+01	3.78e+01	3.19e+01	3.19e+01	2.69e+01	2.69e+01	2.69e+01	2.69e+01	1.35e+01	9.55e+00	5.63e+00	3.58e-07	Pred. No.

87 4.1 535 20 W11255 Hippocampus calcium/c 87 4.1 738 4 R20192 ADH complex protein (87 4.1 738 3 R13993 A.altocetigenes membr 88 4.1 914 178 92522 Pyrodictium occultum 87 4.1 1078 28 W38274 Human parathyroid calcium r 87 4.1 1078 20 W11889 Parathyroid calcium r 87 4.1 1088 14 R70633 Fungus-infected G.lem 87 4.1 1088 14 R72398 Glucan Lyase 1. 87 4.1 1088 14 R72398 anino acid sequence of the VH re 88 4.1 3588 7 R34712 Bactilus subtilis srf 87 4.1 1358 7 R34712 Bactilus subtilis srf 88 4.1 3588 7 R34712 Bactilus subtilis srf 89 4.1 3588 7 R34712 Bactilus subtilis srf 80 4.0 134 10 R54049 Sequence of the VH re 81 4.0 134 20 W01526 Monoclonal antibody z 82 4.0 134 24 W24986 Monoclonal antibody z 83 812463 HLLA-B53 exon. 84 379 13 R64159 Human elastase inhibi 85 4.0 379 17 R94367 Human elastase inhibi 86 4.0 379 17 R94367 Alpha-1,6-glucan-6-gl 87 4.0 1091 14 R70634 Feline zona pellucida 88 4.0 1091 14 R70634 Feline zona pellucida 89 4.0 1091 14 R70634 Feline zona pellucida 80 4.0 1091 14 R70634 Feline zona pellucida 81 3.9 313 0 R55194 Porcine zona pellucida 82 84 3.9 1356 5 R26999 Novel type III RTK en september	4 4 5	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19
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Best Local :
        WO8809386-A.
01-DEC-1988.
27-MAY-1987; FR-007577.
29-MAY-1987; FR-007577.
(DVAL/) DE LA VAILGE BS.
Auffray C, Behar G, Billa
WPI; 88-353959/49.
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A cDNA library was prepared in lambda gt10 from mRNA isolated from ovaries of 3-4 month old cats. Plaques were screened using a mixture of probes encoding porcine ZPA, ZPB and ZPC proteins. Positive clones were analysed further by Southern hybridisation using the porcine probes and clones encoding feline ZPA, ZPB and ZPC proteins were identified. The deduced amino acid sequence (R55200) from the feline ZPA clone was approximately 75% homologous to canine ZPA protein.
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Cat; feline; zona ro''
Felis Ar-
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Harris JD, Hsu KT,
WPI; 94-183156/22.
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larity 30.2%;
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te; histocompatibility complex clasent length polymorphism (RFLP); pro
                                                                                                                                                                                                                                                                                                                                                                                                                             label=alpha 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein"
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                            Bourlet Y.;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sour tastes
Disclosure; Page 34; 50pp; English.
The sequence is that of bovine rod transducin. The sequence was compared to that of bovine cone transducin and a rat novel taste cell specific guanine nucleotide binding protein, gustducin, alpha subunit. Fragments of the protein possessing at least one ligand/antiligand binding activity or immunological property specific to antiligand binding activity or immunological property specific to antiligand binding activity or immunological property specific to antiligand binding activity or immunological property specific to the protein property specific to antiligand binding activity or immunological property specific to the protein pr
Rat gustducin alpha subunit.
Taste modifying agent; ligand;
taste receptor cells; sweet; b;
Rattus rattus.
W09321337-A.
                                                                                                                                                                                    R42424 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gustducin are taste modifying agents taste receptor cells to modify taste, bitter, salty or sour tastes.

See also R42405-36.
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                                                                                                                                  24-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine rod transducin.
Taste modifying agent; ligand;
taste receptor cells; sweet; bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R42426
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WPI; 93-35174
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(MARG/) MARGOLSKEE R F.
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20; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 41.0% 16; Conservative
                                                                                                                                                                                                                                                                                                227
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llarity 30.8%;
Conservative
                                                                                                                                  (first
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Pred.
8; M
                                               d; antiligand; binding
bitter; sweet; salty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d; antiligand;
bitter; sweet
                                                                                                                                                                                    AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          igand; binding activity; taste;
sweet; salty; sour; gustducin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
1.35e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ø
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9.55e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sweet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for identifying taste eet, bitter, salty or
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Best Local S
Matches 2
                                                                                                                                                                  Query Match
                                                                                                                                                                                                             of animals and monoclonal antibody development.

Claim 3; Page 2; 13pp; Japanese.

Probes comprising part of the DNA sequence encoding the protein can be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HLA-C antigen. See also R12466 (same patent) and J03112486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a rat novel taste cell specific guanine nucleotide binding protein, gustducin, alpha subunit. Fragments of the protein possessing at least one ligand/antiligand binding activity or immunological property specific to gustducin are taste modifying agents which can be delivered to taste receptor cells to modify taste, e.g. mimic or inhibit sweet, bitter, salty or
           15-MAR-1995 (first entry)
Canine zona pellucida CZP2
                                                                                                                                                                                                       for the HLA-C antigen. and J03112487.
                                                                                                                                                                                                                                                                                                       N-PSDB; Q12116.
                                                                                                                                                                                                                                                                                                                     WPI; 91-182989/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New gustducin alpha subunit protein modifying agents which mimic or inhi
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Canine;
                                   R60101 standard;
R60101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also R42405-36.
Sequence 354 AA;
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09-APR-1992;
                                                                                                                                                                                                                                                                                            HLA-C gene, DNA probe and transformant cells -
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                                                                                                                                                                                                                                                                                                                                                                                                        MHC; class I.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte antigen; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R12465 standard;
R12465;
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                                                                                                                    180
                                                                                                                                                                                                                                                                                                                               22-SEP-1989; JP-247695.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dsaayy-Indldrltapgyvpneqdvlhsrlktt-giietqfsfk-dlnfrmfdvgggrs 206
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                                                                                           KPGYLEAT-VDWFRRYKVPDGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                 exon Cb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Page 32-3; 50pp; English
                                                                                                                                          h 4.3%;
Similarity 50.0%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                             366
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US-868353
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                                                                                                                                                                                             8
                                             Protein; 713
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pellucida; ZP; CZP2; contraceptive; vaccine;
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No. 2.69e+01
                                                                                                                                       2.69e+01;
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                                                                                                                                                                  Length 366;
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                                                                                                                                                                                                                                                                                             for immunisation
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P80911 stand
P80911;
18-SEP-1990
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J0618976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R55198'standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA sequence encoding canine zona pellucida CZP2 the prodn. of a canine contraceptive vaccine antigen Claim 1; Page 8-10; 10pp; Japanese.
The CZP2 DNA (Q70072) was prepd. by the cloning of CZ Q81700 using the primers given in Q70073-74, CZP2(1-6
                                                                                                                                                                                      used as probes in Southern hybridisations. Sequences coding for canine ZPA and ZPC proteins were obtained (Q65608 and Q65609, respectively). R55198 is the deduced amino acid sequence for Sequence 715 AA;
                                                                                                                                                                                                                                           library in lambda gtl1 was screened using antibodies raised against
heat solubilised canine zona pellucida. The largest candidate clone
was used to rescreen the library and to isolate clones which were
                                                                                                                                                                                                                                                                                                                                            Use of
                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q65608
                                                                                                                                                                                                                                                                                                                                                                         WPI:
                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-1993; U10851.
09-NOV-1992; US-973341.
29-JAN-1993; US-012990.
                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-1994.
06-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dog; canine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canine zona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The CZP2 DNA (070072) was prepd. by the cloning of CZP2(75-520) 081700 using the primers given in 070073-74, CZP2(1-65) - 081804 using the primers given in 070082-83, CZP2(42-103) - 081803 using the primers given in 070082-83, CZP2(42-103) - 081957 using the primers given in 070079-81 and CZP2(487-713) - 081957 using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 94-259553/32.
                                                                                                                                                                                                                                                                                     A commercially available
                                                                                                                                                                                                                                                                                                                              reproducible transient
                                                                                                                                                                                                                                                                                                                                                                                   Harris JD,
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                                                                                                                                                                                                                                                                                                                                                                                                  (ZONA-)
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                                                                                                                                                                                                                                                                                                                 emale mammals
                                                                                                                                                                                                                                                                                  laim 40; Page 88-90; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 FHMVVEVPRWSNAKMEIATK-DPLNPIKQDVKKGKLRYVANLFPYKGYIWNYG
                                                                               44
                                                                                            frmtvkc-hysrddllintnvqslpppvasvrpgplalilqtypdksylrpyg
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                        standard;
                                                                                                                               h 4.3%;
Similarity 30.2%;
16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  ZONAGEN INC.
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; zona pellucida; ZPA; immunocontraception.
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Conservative J
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                        protein;
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Pred. No.
12; Misma
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12; Misma
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2.69e+01;
-hes 23;
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ches 23;
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Consensus

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Best Local :
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23-AUG-1991; US-749451.
11-FEB-1992; US-934161.
21-AUG-1992; US-934161.
21-EB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-141248.
19-AUG-1994; US-292827.
21-OCT-1994; US-292827.
21-OCT-1994; US-353784.
(BGHM) BRIGHAM & WOMENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used for modulating cylulual seases transplants or auto-inmune diseases transplants or auto-inmune diseases Example 9; Fig 4; 60pp; English.

The concensus sequence is derived from a total of 23 HLA-A, B, C sequence concensus sequences in the three extrecellular domains (alpha-1).

The protein sequences in the three extracellular domains (alpha-1) and alpha-3) are shown. The example concerned the effect cellular domains (alpha-1) and alpha-3) are shown.
The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The proteins, nucleic acids and antibodies may be used to treat
                                                                    DNA encoding calcium receptor polypeptide(s) therapeutic purposes, e.g. hyperparathyroidism Claim 20; Columns 133-142; 174pp; English. The present sequence is rat kidney cell calcium
                                                                                                                                                        Brown
                                                                                                                                                                      (BGHM )
                                                                                                                                                                                                                                                                                                                                                               Rattus sp. -
US5688938-A
                                                                                                                                                                                                                                                                                                                                                                                                    Rat kidney cell calcium receptor 3A (RakCaR 3A). Rat kidney cell calcium receptor 3A; RakCaR 3A;
                                                           receptor 3A (RakCaR 3A)
                                                                                                                                 N-PSDB; T95860
                                                                                                                                                                                                  08-DEC-1994;
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(STRD) Leland Stanford
Krensky AM, Parham P, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 qlra-ylegtcvewlrry-lengk 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide corresp.
used for modulating o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 88-235147/33.
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30-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO8805784-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA-A2 epitopes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 RLKPGYLEAT-VDWFRRYKVPDGK 199
                                                                                                                                                                                                                                                                                                                                                                                           lcium
                                                                                                                                           98-008040/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide corresp. to major histocompatibility antigen refor modulating cytotoxic T-lymphocyte activity in e.g.
                                                                                                                                                          EM,
                                                                                                                                                                      NPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                          homeostasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regions
                                                                                                                                                    PS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   egions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.28;
larity 50.08;
Conservative
                                                                                                                                                                     & WOMENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="alpha-2 region|
|81..272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ce of peptides which constitute of a class I HLA molecule extracellular domains alpha-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="alpha-3 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="alpha-1 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                     Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                       hyperparathyroidism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jr Univ
                                                                                                                                                                                HOSPITAL.
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Pred.
                                                                                                                                                       JE, Hebert SC;
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. 3.19e+01;
                                                                                                                                                                                                                                                                                                                                                                                       osteoporosis.
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                                                                                                 and
                                                                                                             useful
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                                                                                              osteoporosis
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Best Local S
Matches 1
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                                  Pyrodictium occultum DNA polyn DNA pol; base pair; thermally polymerase chain reaction; di pyrodictium occultum DSM2709.
                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor roteins activities, preferably disorders of calcium homeostasic hyperparathyroidism and necestaric calcium homeostasic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification includes details of molecules that can modu one or more inorganic ion receptor activities, and antibodies antibody fragments targetted to inorganic ion receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine
Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W38272
W38272
                                                                                                                       12-JUL-1996
                                                                                                                                           R92524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor 1 (BoPCaR 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding calcium receptor polypeptide(s) - therapeutic purposes, e.g. hyperparathyroidism Claim 4; Columns 107-116; 174pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders by modulating activities, preferably of hyperparathyroidism and Sequence 1079 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T95857
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                                                                                                                                                                                                                                                                                         232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 NEKGQYISPFHD-IPIYADKDVFHMVVEVPRWSNAKMEIA-TKDP-LNP-IKQDVKK
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                                                                                                                                                                                                                                                              NEKGQYISPFHD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) BRIGHAM & WOMENS HOSPITAL.
-) NPS PHARM INC.
-M, Fuller FH, Garrett JE, Hebert
                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parathyroid cell calcium receptor 1 (BoPCaR 1).
parathyroid cell calcium receptor 1; BoPCaR 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                  19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                   1085 AA;
                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-353784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-292827
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                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                           4.2%;
                                                                                                                 entry)
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disorders of calcium h
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Pred.
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Pred.
16;- M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO ;
                                                                       gene PCR product.
e; exonuclease act
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3.78e+01;
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3.19e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoporosis
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and ost
                                                                                                                                                                                                                                                                                                                                                                   Length 1085;
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                                                                     activity;
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stasis, e.
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Location/Qualifiers

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Best Local Similarity 24.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.18;
Best Local Similarity 21.68;
                                                                                                                                                                                                                                                                                         Disclosure; Page 5; 5pp; German.

Disclosure; Page 5; 5pp; German.

The DNA may be used as a hybridisation probe for detecting the HLA B27 gene, eg for assessing susceptibility to rheumatic disorders such as ankylosis spondylitis, or may be used to transform cells for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27.
                          us-APR-1991 (first
Sequence encoded by
antigen HLA-B 27.
                                                                                      T 14
P70155 standard;
P70155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       occultum and produce thermostable DNA polymerase. Also disclosed are DNA polymerase genes which hybridise to the above genes. Sequence 138 AA;
                                                          10-MAR-1993
03-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR performed on Pyrodictium occultum chromosomal DNA. Two full lenguenes encoding a 914 amino acid and an 803 amino acid DNA polymerase were later identified. The genes are derived from Pyrodictium
                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     such DNA, antigen or antibody
                                                                                                                                                                                                                                                                                                                                                                                                                 DNA coding for antigen HLA B27 - and diagnostic reagents contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BEHW ) BEHRINGWERKE AG.
Riethmuller G, Meo T, Weiss E, Szots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rheumatic disorder; genetic ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 13; 23pp; Japanese
R92524 and R92525 are proteins encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUN-1994; 150591.
09-JUN-1994; JP-150591
             Ankylosing spondylitis; rheumatic disorder; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-1985; DE-542024.
21-DEC-1985; DE-545576.
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Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P70590 standard;
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NPI; 96-072342/08.
                                                                                                                                                                 147
                                                                                                                                                                                        125 lnedlsswtaadtaagitqr-kweaarvaeqlra-ylegecvewlrry-lengk 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ypsiikrw-nlsyetvnpvycpesklvevpdvghkvcmsipgltsqivgll 52
                                                                                                                                                                                                                                                                              n human serum, or to pro
for use in immunoassay.
337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the human
                                                                         (revised)
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                                                                                                       protein;
                                       genomic DNA encoding human histocompatibility
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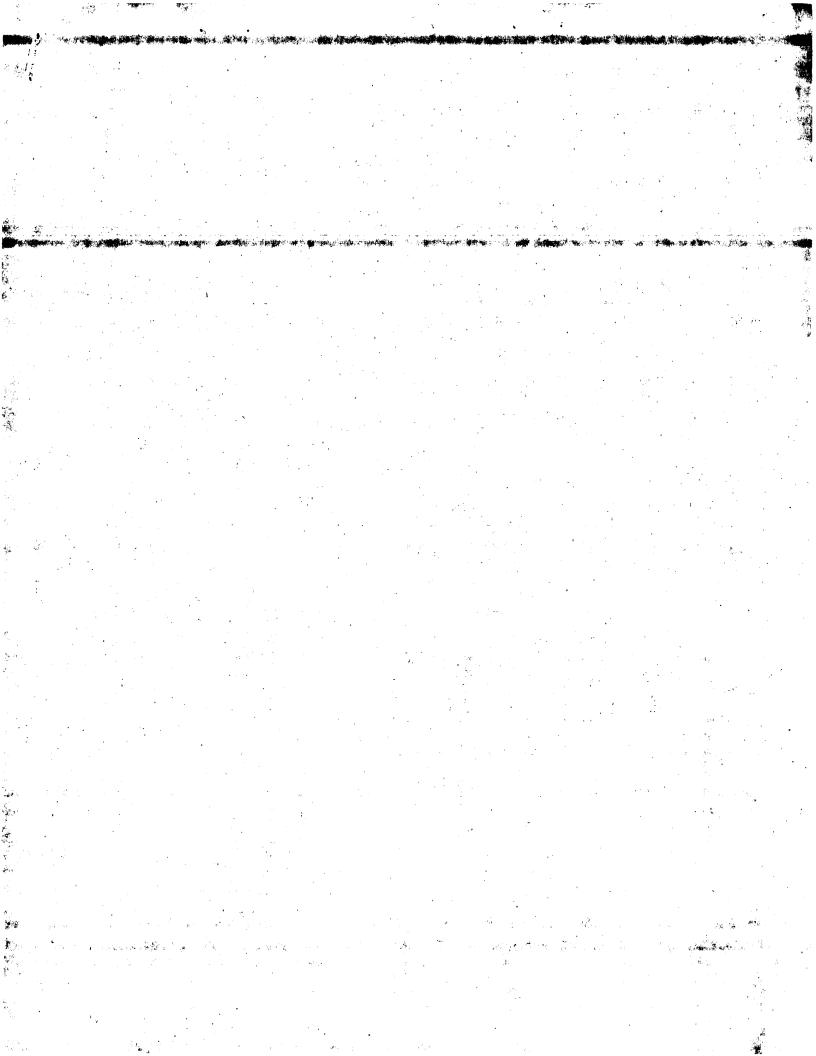
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R12466 standard;
R12466;
                                                                                                                       be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HLA-C antigen. See also R12465 (same patent) and J03112486 and J03112487.
                                                                                                                                                                                           of animals, and monoclonal antibody development. Claim 4; Page 2; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; p6; 13pp; German.
THE DNA may be used to detect the HLA-B 27 gene (opt. mutated human genetic material. The HLA-B 27 may be used to detect at B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Szots H, Weiss E, Dorner C, WPI; 87-171469/25.
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21-DEC-1985;
                                                                                                           Sequence
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181 GYLEAT-VDWFRRYKVPDGK
                 robes comprising part of the DNA sequence encoding the protein
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******* ***** (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Sep 17 16:57:21 1998; MasPar time 3.93 Seconds 518.696 Million cell updates/sec

Description:
Perfect Score:
Sequence: >US-08-741-437-1 (1-289) from US08741437.pep

Scoring table: PAM 150 Gap 11

Searched: 77021 seqs, 7058996 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.457; Variance 133.821; scale 0.235

SUMMARIES

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LENGTH: 286 amino acids		TELEFAX: (508) 927-1705	E: (50	TELECOMMUNICATION INFORMATION:	REFERENCE/DOCKET NUMBER: NEB-105-PCT	BER: 30	NAME: WILLIAMS, GREGORY D.	ū	T-199	APPLICATION NUMBER: US 08/329,721	PRIOR APPLICATION DATA:	CLASSIFICATION:	FILING DATE:	APPLICATION NUMBER; PCT/US95/13662A	ATA:	PatentIn	SYSTEM:	COMPUTER: IBM PC Compatible	_	ä	9	۲	••	BEVE	2 TOZER ROAD	ADDRESSEE: NEW ENGLAND BIOLABS, INC.	Š	R OF SEQUENCES:	OF INVENTION: LITORALIS	INVENTION: , PYROPHOSPHATASE OBTAIN	NVENTION: PURI	SEARS, Lauren E	SLATKO,	CANT: LENNOX, Tricia	INFORMATION:	Sequence 3, Application PC/TUS9513662A		Sequence 3, Application PC/TUS9513662A			A CONTRACTOR OF THE CONTRACTOR	YYYYYY	PCT-US95-13662A-3 STANDARD; PRT; 286 AA.	1

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4 FSTEERAAPFSLEYRVELKNEKGQYISPFHDIPIYADKD--VFHMVVEVPRWSNAKMEIA 61
                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                   FILING DATE: 25-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
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REFERENCE/DOCKET NUMBER: 30
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CLASSIFICATION:
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l Similarity 53.0%;
l51; Conservative
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PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
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60; Mismatches 64
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Best Local Similarity 36.9%;
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                                              TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (508) 927-17
INFORMATION FOR SEQ ID NO:
                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FITLE OF INVENTION:
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                           REGISTRATION NUMBER: 309
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                            ENGTH:
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176 AA; 20659 MW; 160121 CN;
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           amino acid
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                              179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 TOZER ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEARS, Lauren E.
                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEW ENGLAND BIOLABS,
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unknown
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927-1705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tricia L.
Barton E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS LITORALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PURIFIED THERMOSTABLE INORGANIC
                                                                                                                                                                                                                                                                           PCT/US95/13662A
                                                                                                                                            3090
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Pred. No. 2.28e-07
20; Mismatches 30
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          Matches
                                      Query Match
Best Local :
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SEQUENCE 179 AA; 20465 MW; 177070 CN;
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                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 KDVNAHLLDEIANFFSTYKILEKKETKVLGWEGKEAALKEIEVSI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 DNDPIDVCEIGSKVCARGEIIGVKVIGILAMIDEGETDWKVIAINVDDPDAANYNDINDV 175-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.7%;
Local Similarity 30.5%;

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                                                                                                                                     TOPOLOGY: un
MOLECULE TYPE:
UENCE 164 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NE
TELECOMMUNICATION INFORMATION:
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FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: unl
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       Similarity
28; Conser
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                                                                                                                                                                                                                                                                                                   164 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLATKO, Barton E.
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                                                                                                                                                                                                           unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (508) 927-5054
                                                                                                                                        protein
18792 MW;
                                      7.2%;
33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GREGORY D.
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                                                                                                                                        MW; 129342 CN
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Score 154; DB 2; Le
Pred. No. 1.07e-04;
18; Mismatches 35;
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Pred. No. 1.23e-05;
31; Mismatches 38
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                                                                  Length 164;
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                                            113 EDLPOHKLKEIAHFFERYKDLOGK 136
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                                                                                                           Match 7.1%;
Local Similarity 37.1%;
                                                                                                                                                                                                                                                     TELEFAX: (508) 927-170 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                         MOLECULE TYPE: protein 
JENCE, 263 AA; 29712 MW; 339305 CN;
                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (508), 927-5054
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: '25-OCT-199
ATTORNEY/AGENT INFORMATION
NAME: WILLIAMS, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LENNOX, Tricia L. APPLICANT: SLATKO, Barton E. APPLICANT: SEARS, Lauren E.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
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                             CGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIN 173
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                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: unkl
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US (FILING DATE: 25-OCT-1994
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                                                                                                                                                                                                                                        LENGTH:
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 163
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                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASSACHUSETTS
                                                                                                                                                                                                                                     263 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                     GREGORY D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT/US95/13662A
                                                                                            18;
                                                                                                           Score 151; DB 2;
Pred. No. 1.91e-04;
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                                                                                          Mismatches
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             XXXXXX
                                          US-08-127-954-165
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                                                                                                                                 123 VNDL-PELLKAQIAHFFEHYKDLEKGK 148
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                                                                                                                                                                                          65 DGDPVDV-LVPTPYPLQPGSVIRCRPVGVLKMTDEAGEDAKLVAVPHSKL-SKEYDHIKD 122
                                                                                                                                                                                                                              Match 5.5%;
Local Similarity 32.2%;
nes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amin-
                                                                                                                                                                                                                                                                                          TOPOLOGY: un MOLECULE TYPE: QUENCE 175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: NITELECOMMUNICATION INFORMATION TELEPHONE: (508) 927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0: FILING DATE: 25-OCT-1994 ATTORNEY AGENT INFORMATION:
                                                                                                  VKRLKPGYLEATVD-WFRRYK-VPDGK 199
                                                                                                                                                            DNDPIDVCEIGSKVCAR-GEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIND 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application PC/TUS9513662A
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                                                                                                                                                                                                                                                                                                                         unknown
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                                                                                                                                                                                                                                                                                       protein
19572 MW; 155266 CN;
                                                                                                                                                                                                                                                                                                                                      unknown
                                        STANDARD;
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PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
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                                                                                                                                                                                                                          Score 118; DB 2;
Pred. No. 9.80e-02;
20; Mismatches 33
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                                     PRT;
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                                     182 AA.
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                                                                                                                                                                                                                                                                                                       147 IDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEAT-VDWFRRYKVPDGK 199
                                                                                                          Sequence 146, Application US/08127954 Patent No. 5451512
                                                                                                                                                                                                                                                                                                                                     126 LNEDLRSWTAADMAAQITQR-KWETAHEAEQLRA-YLEGTCVEWLRRY-LENGK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 165, Application US/08127954
                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (510) 814-29/
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Apple,
              TITLE OF INVENTION:
                                             APPLICANT:
                                                                         APPLICANT:
                                                              APPLICANT:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 182 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Nutley
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                                                         Bugawan;
                                                                       Apple, Raymond J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                   STANDARD;
Locus DNA Typing
173
                        Methods and Reagents for HLA Class I A
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CORRESPONDENCE ADDRESS:

PRT;

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Query Match 4.8%; Score 103; DB 1; Best Local Similarity 25.9%; Pred. No. 1.45e+00; Matches 14; Conservative 17; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 165, Application US/0812795, Patent No. 5451512
                                                                 MOLECULE TYPE: DNA (genomic)
UENCE 182 AA; 21175 MW; 151183 CN;
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,954
                                                                                                                                                                                                                                                                                                        Petry, .Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bugawan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apple, Raymond J.
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) Kingsland Street
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173
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 19;
                                   Length 182
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Indels
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 IDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEAT-VDWFRRYKVPDGK 199
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                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application
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Local Similarity 24.18;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SENCE 182 AA; 21058 MW; 149365 CN;
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LENGTH: 182 amino acids
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TELECOMMUNICATION INFORMATION:
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NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                         APPLICANT: Margolskee, Robert F.
TITLE OF INVENTION: Gustducin Materials and Methods
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                 SOFTWARE:
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                                           PatentIn Release #1.0, Version #1.25
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19920409
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               US/07/868,353A
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                                                                                                                                                                                                                                                                 O'Toole, Gerstein, Murray &
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Pred. No. 2.06e+00;
17; Mismatches 20
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Best Local
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US-07-868-353A-15
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Local Similarity 30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID: NO: SEQUENCE CHARACTERISTICS: LENGTH: 350 amino acid
        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         tent No. 5688662
ENERAL INFORMATION: Margol
                                                                                                                                                SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                 TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                            APPLICANT: Margolskee, TITLE OF INVENTION: Gus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                      ATTORNEY/AGENT
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                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                             TELEFAX: (312) 984-9740
TELEX: 25-3856
                                                                              TORNEY/AGENT INFORMATION:
NAME: No. 5688662and, Gret
REGISTRATION NUMBER: P-35,
                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           STREET: Two Fin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                           APPLICATION NUMBER: FILING DATE: 19920
                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                 ZIP: 60603
                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshal
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25-3856
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                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                              ee, Robert F.
Gustducin Materials and Methods
                                                                                                                                                                                                                                                                                             1; O'Toole, Gerstein, Murray &
                                                                                                                                                            Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d, Greta E
P-35,302
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Pred. No. 5:
17; Mismatc
                                                                                                                                      US/07/868,353A
                                                                                   Greta E.
P-35,302
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5.83e+00;
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MOLECULE TYPE:

protein

TYPE: AMINO ACID

SEQUENCE

FEATURE: /note= "Positions indicated as Xaa OTHER INFORMATION: /note= "Positions indicated as Xaa OTHER INFORMATION: represent nonconserved amino acids." rewre 354 AA: 40403 MW; 673372 CN;

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Query Match
Best Local Similarity
Conserv
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ID US-08-127-954-142
              Query Match
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                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bugawan, Teodórica L.
APPLICANT: Erilch, Henry A.
TITLE OF INVENTION: Methods and Reagents
TITLE OF INVENTION: Locus DNA Typing
                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
JENCE 182 AA; 21202 MW; 160101 CN;
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 88
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 07110-1199
                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                             FILING DATE
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                                                                                                                                     LENGTH:
                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                     STRATION NUMBER: 35,321
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llarity 32.3%;
Conservative
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4.3%;
27.7%;
                                                                                                   single
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Pred. No. 4.14e+00;
15; Mismatches 24;
Score 92; DB 1; Length 182; Pred. No. 9.73e+00;
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Best Local Similarity

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Best Local Similarity 25.9%;
Matches 14; Conservative
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                                                                         US-08-127-954-161
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                                                                                                                                       147 IDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEAT-VDWFRRYKVPDGK 199
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                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (510) 814-2977 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
JENCE 182 AA; 21163 MW; 148760 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: -436
ATTORNEY/AGENT INFORMATION:
. NAME: PELTY, DOUGLAS A.
REGISTRATION NUMBER: 35,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Methods and Reag TITLE OF INVENTION: Locus DNA Typing NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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Erlich, Henry
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Pred. No. 9.73e+00;
15; Mismatches 21
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Matches 14; Conser
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                                                                                                                                                       Sequence 160,
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                                                                                                                               Sequence 160,
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                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
JENCE 182 AA; 21125 MW; 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 88
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                       CORRESPONDENCE ADDRESS:
                                    NUMBER OF SEQUENCES:
                                                                         PPLICANT:
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                                              TLE OF INVENTION:
                                                                                   PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New Jo
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"LICANT: Erlich, Henry A.

"LE OF INVENTION: Methods and Reagents for HLA Class I A.

"LE OF INVENTION: Locus DNA Typing"
              DDRESSEE:
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AL INFORMATION:
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larity 25.9%;
Conservative
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 E: Hoffmann-La Roche Inc
340 Kingsland Street
                                                                                                                               Application US/08127954
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                                                                    Bugawan, Teodori
Erlich, Henry A.
                                                                                             Apple, Raymond J.
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510) 814-2977
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                                               Locus DNA Typing
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                                                           Methods and Reagents
                                                                                 Teodorica L
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Pred. No. 9.73e+00;
15; Mismatches 21
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                                                            for HLA Class I A
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Best Local Similarity 25.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                  Sequence 140, Application US/08127954
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                                                                                                                                                                                                                                                                                  Sequence 140, Application US/08127954 Patent No. 5451512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (510) 814-29: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,954
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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JENCE. 182 AA; 21022 MW; 147718 CN;
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LENGTH: 182 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
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NAME: Petry, Douglas A.
                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                APPLICANT: Bugawan, Teodori
APPLICANT: Erlich, Henry A.
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Locus D
NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                             NERAL INFORMATION:
APPLICANT: Apple, Raymond J.
APPLICANT: Bugawan, Teodoric
TTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
         APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 436
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O Kingsland Street
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                                                                                                                                                                                                            Locus DNA Typing
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                                 US/08/127,95
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Pred. No. 9.73e+00;
15; Mismatches 2:
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Length 182;

4. Gaps

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CC REGISTRATION NUMBER: 35.321
CC REFERENCE/DOCKET NUMBER: 8873
CC REFERENCE/DOCKET NUMBER: 8873
CC REFERENCE/DOCKET NUMBER: 8873
CC FILEFONMUNICATION INFORMATION:
CC TELEFAX: (510) 814-2974
CC TELEFAX: (510) 814-2977
CC TELEFAX: (510) 814-2977
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CC TEMOTH: 182 amino acids:
CC TYPE: amino acids:
CC TYPE: DNA (genomic)
CC TYPE: DNA (genomic)
CC TOPOLOGY: 11near
CC MOLECULE TYPE: DNA (genomic)
SQ SEQUENCE 182 AA; 21:61 MW; 16:123 CN;
SQ SEQUENCE 182 AA; 21:61 MW; 16:123 CN;
Query Match
Best Local Similarity 27.7%; Pred: No. 9.73e+00;
Matches 13; Conservative 13; Mismatches 17; Indels 4; Gaps 4;
Matches 13; Conservative 13; Mismatches 17; Indels 4; Gaps 4;
Matches 13; Tenschtvaeplara-ylegtcvewlerry-lengk 176
Db. 133 WTAADMAAQTTKH-KWEAAHVAEPLRA-YLEGTCVEWLERRY-LENGK 176
Db. 133 WTAADMAAQTTKH-KWEAAHVAEPLRA-YLEGTCVEWLERRY-LENGK 176
Db. 134 WKVIAINVDDPDAANVNDINDVKRLKPGYLEAT-VDWFRRYKVPDGK 199
Search completed: Thu Sep 17 16:57:40 1998.
Job time: 19 secs.
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ALTERNATE_NAMES
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                                                                           154-159,137-143
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8,56,58,78,89,93,
15,117,120,147,
52,154,192,193
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The structural basis for pyrophosphatase catalysis
  #length
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New crystal forms of e. coli and
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inorganic pyrophosphatase (EC 3.6.1.1)
B - yeast (Saccharomyces cerevisiae)
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115,117,120,147,
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93 #site Glu, Lys, Glu, Arg, Tyr, Tyr, Asp,
Asp, Lys, Tyr, Lys #label ASA
#length 283 #molecular-weight 31941 #checksu
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llarity 53.0%;
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Cooperman, 'B.S.; Goldman, A.
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A68201
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(Saccharomyces cerevisiae)
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the Brookhaven Protein Data
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Pred. No. 1.56e-166;
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                                                Asp, Asp,
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                                                                                                                                                                                                                                                                                                                                                                                   Crystallogr. Rep. (Transl. Kristallografiya) (1996) 41:84
Structure of inorganic pyrophosphatase from e. coli and its
complex with a mn2+ ion at 2.2 angstroms resolution.
                                                                       Kankare, J.; Neal, G.S.; Salminen, T.; Glumhoff, Cooperman, B.S.; Lahti, R.; Goldman, A. Protein Eng. (1994) 7:823
The structure of e. coli soluble inorganic pyropl
                                                                                                                                                                                                                                                                          Acta Crystallogr. (1995) D51:399
New crystal forms of escherichia coli and saccharomyces cerevisiae soluble inorganic pyrophosphatases.
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X-ray structure of yeast inorganic pyrophosphatase complexed
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     Baykov, A.A.; Shestakov, A.S.
Eur. J. Biochem. (1992) 206:463
                                                                                                                                                                                Crystal structure of inorganic pyrophosphatase from thermus
                                                                                                                                                                                                     H.; Samejima, T.; Kuranova, I.
Protein Sci. (1994) 3:1098
                                                                                                                                                                                                                         Teplyakov, A.; Obmolova, G.; Wilson, H.; Samelima. T : Kurarowa
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S.S.; Popov, A.N.; Rubinskiy, S.V.; Vainshtei
zarova, T.I.; Kurilova, S.A.; Vorobyova, N.N.;
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Pred. No. 1.56e-166;
60; Mismatches 64;
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iy, S.V.; Vainshtein,
                                                                           pyrophosphatase
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A.V.; Wilson,
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Determination: X-ray diffraction
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Eur. J. Biochem. (1974) 47:57
Yeast inorganic pyrophosphatase:
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Crystal structure of mnpi complex of yeast inorganic
pyrophosphatase at 2.35 angstroms resolution (Russian).
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The growing of crystals of inorganic pyrophosphatase yeast with metal ions and phosphate (Russian).
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H.; Samejima, T.; Kuranova, I.
Protein Sci. (1994) 3:1098
Crystal structure of inorganic pyrophosphatase
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X-ray structure of yeast inorgan
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                                                              Teplyakov, A.; Obmolova, G.; Wilson,
                                                                                             Acta Crystallogr. (1995) D51:399
New crystal forms of escherichia coli and saccharomyces
cerevisiae soluble inorganic pyrophosphatases.
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Terzyan, S.S.; Popov, A.N.; Rubinskiy, S.V.; Vainshtein,
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Eur. J. Biochem (1974) 47:57
Yeast inorganic pyrophosphatase:
Resolution: 2.4 angstroms
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Eur. J. Biochem. (1992) 206:463
Two pathways of pyrophosphate hydrolysis
yeast inorganic pyrophosphatase.
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The mechanism of action of yeast
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Kuranova, I.P.; Sokolov, V.I.
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The growing of crystals of inorganic pyrophosphatase yeast with metal ions and phosphate (Russian).
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Crystal structure of mnpi comp
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Similarity 52.8%;
150; Conservative
 Similarity
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31-Dec-1991 #sequence_revision
05-Sep-1997
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inorganic pyrophosphatase (EC 3.6.1.1) -
marxianus var. lactis)
                                                                           #superfamily hydrolase
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Pred. No. 5.83e-166;
58; Mismatches 68;
 Score 1022; DB 1;
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X-ray structural investigation of inorganic pyrophosphatase of baker yeast. II. phase calculation and structure model
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X-Ray diffraction study of inorganic pyrophosphatase from
baker's yeast at the 3 angstroms resolution (Russian).
                                                                         x-ray structural investigation of inorganic pyrophosphatase of baker yeast. I. Growing of crystals, production of derivatives and determination of the heavy atom positions
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of yeasts. II. calculation of phases and structural model
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Makhaldiani,
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Protein
  V.V.;
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in Data Bank,
     Voronova,
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  A.A.; Kuranova
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Heitmann, P.;
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 ch 47.5%;
l Similarity 51.8%;
147; Conservative
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Covalent structural analysis of yeast inorganic
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X-ray structural investigation of inorganic-pyrophosphatase of yeasts. i. growth of crystals, formation of derivatives, and determination of the positions of their heavy atoms.
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kl. Biochem. (1978) 240:200
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                                                                                       h 45.7%;
Similarity 57.3%;
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Cooperman, B.S.; Goldman, A.
Structure (London) (1996) 4:1491
                                                                                                                                                                                                                                                                                                                                                                                                                  hydrolase; manganese; pyrophosphate phosphohydrolase
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New crystal forms of e. coli and s.
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inorganic pyrophosphatase (EC 3.6.1.1) metal complex,
B, fragment 1 - yeast (Saccharomyces cerevisiae)
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                                                                                   Score 976; DB 5; I
Pred. No. 2.68e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSEYTTREVGALNTLDYQVYVEKN-GTPISSWHDIPLYANAEKTILNNVVVEIPRWTQAKL 59:
                                                                                                                                                                                                                                                                             LKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVTKKTNG
                                                                                                                                                                                                                                                                                              HMPGLIRATHEMFRIYKIPDGKPENSFAFSGECKNRKYAEEVVRECNEAWERLITGKTDA 238
                                                                                                                                                                                                                                                                                                                                               PIDVCEIG-SKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                EITKEATLNPIKODTKKGKLRFVRNCFPHHGYIWNYGAFPQTYEDPNVVHPETKAKGDSD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSGFSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIYA--DKDVFHMVVEVPRWSNAKM 58
                                                                                                                                                                                                                                            KSDFSLVNVSVTGSVAN-DPSVSSTIPPA-QEL-APA-PVDPSVHKWF 282
                                                                                                                                                                                                                                                                                                                                                                                                                 EIATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDND
                                                                                                                                                                                                                KG-ISCMNTTLSESPFKCDPDAARAIVDALPPPCESACTVPTDVDKWF
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Similarity 48.6%;
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    (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-Jan-1995 #sequence_revision
                                                                                        inorganic pyrophosphatase (EC 3.6.1.1)
mitochondrial yeast (Saccharomyces
protein YM8156.09; protein YMR267w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #active_site Arg #status predicted
#length 289 #molecular-weight 32467 #checksum 5076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 formal_name Schizosaccharomyces
                                                            #formal_name Saccharomyces cerevisiae
27_Mar-1992 #sequence_revision 27-Mar-1992 #text_change
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                                              06-Feb-1998
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1-289 ##label KAW
1-289 ##1abel KAW
1-2 PMRI:X54301; NID:g5013; PID:g5014
 M.; Baltscheffsky,
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18:5888
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13-Jan-1995
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##cross-references GB:M81880;
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                                 ##cross-references EMBL:X64200;
                                                  ##residues
                                                              ##molecule_type DNA
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Similarity 48.18;
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Yeast PPA2 gene encodes a mitochondri
pyrophosphatase that is essential f
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hydrolase; mitochondrion
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                                                                                               Richter, O.M.H.; Schaefer, G. Bur. J. Blochem. (1992) 209:351-355
Eur. J. Blochem. (1992) 209:351-355
Cloning and sequencing of the gene for the cytoplasmic inorganic pyrophosphatase from the thermoacidophilic archaebacterium Thermoplasma acidophilum.
                                                                                                                                                                                                                 #formal_name Thermoplasma acidophilum
22-Jan-1994 #sequence_revision 10-Nov
09-Sep-1997
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#length 179
                   hydrolase
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                                                  1-179 ##label RIC
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   #molecular-weight
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Pred. No. 2.99e-124;
51; Mismatches 65;
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NID: g172222;
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                                 NID: 948081; PID: 948082
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     #checksum
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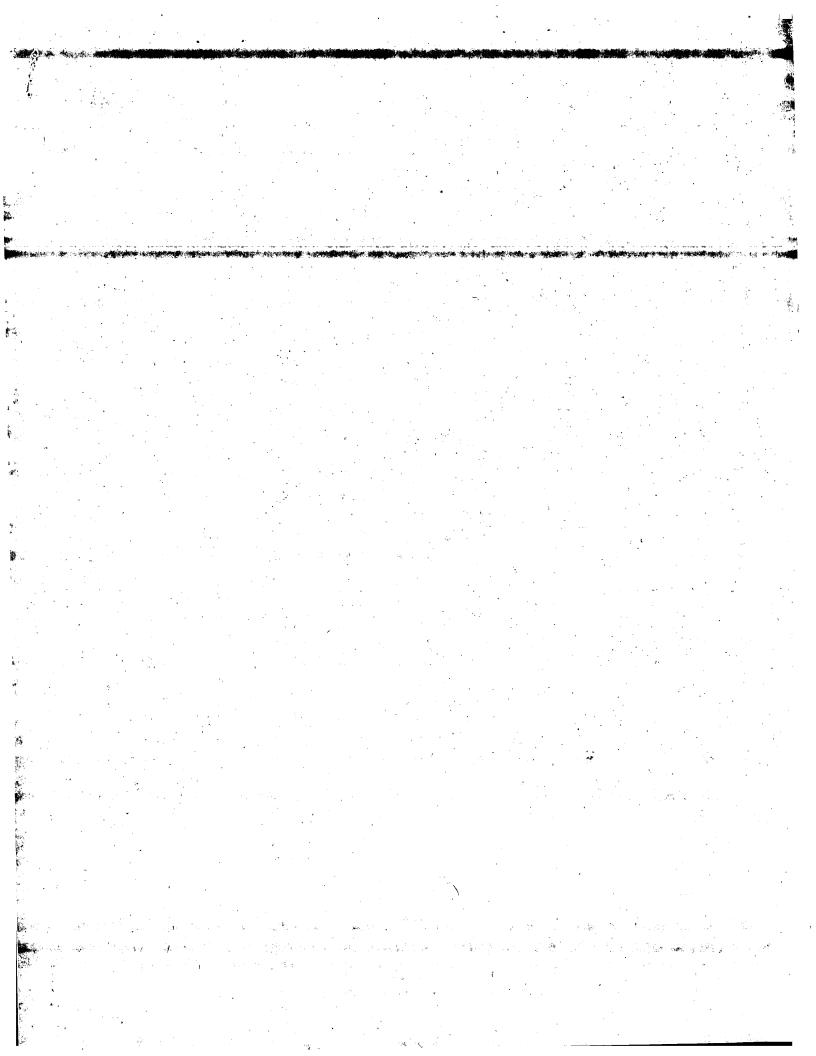
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                                                                                                                    #authors Ichiba, T.; Takenaka, O.; Samejima, T.; Hachimori, A.
#journal J. Biochem. (1990) 108:572-578
#title Primary structure of the inorganic pyrophosphatase from
thermophilic bacterium PS-3.
#across-references MUID:91154162
#acression JX0135
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##residues 1-164 ##label SAT
##experimental_source strain ATCC 12016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 KRLKPGYLEATVDWFRRYKVPDGKPENEFAFNA-EFKDKDFAIDI 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 KRLKPGYLEATVDWFRRYKVPDGK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 EDLPQHKLKEIAHFFERYKDLQGK 136
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                                                                                                   ##molecule_type protein
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Local Similarity 30.5%;
hes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.2%;
Local Similarity 33.3%;
les 28; Conservation
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                                                idues 1-164 ##label ICH
This enzyme is a trimer of identical chains. It catalyzes the hydrolysis of pyrophosphate to orthophosphate in the presence of
                                   divalent metal cations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primary structure, overexpression, characterization and crystallization of inorganic pyrophosphatase from Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Satoh, T.; Ishii, K.; Koyama, M.;
Hachimori, A.; Irie, M.; Samejin
submitted to JIPID, April 1997
                                                                                                                                                                                                                                                                                      pyrophosphate phosphohydrolase
#formal_name thermophilic bacterium PS-3
30-Jun-1992 #sequence_revision 30-Jun-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Bacillus stearothermophilus
28-May-1997 #sequence_revision 18-Jul-1997 #text_change
18-Jul-1997
                                                                                                                                                                                                                                                                                                                                                inorganic pyrophosphatase (EC 3.6.1.1) - thermophilic
bacterium PS-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #active_site Glu #status predicted
#length 164 #molecular-weight 18796 #checksum 5644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JH0271 #type complete inorganic pyrophosphatase (EC 3.6.1.1) - stearothermophilus
                    hydrolase
                                                                                                                                                                                                                                                                         28-Apr-1993
                                                                                                                                                                                                                                                                                                                                                                                  #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 154; DB 2;
Pred. No. 1.37e-07;
18; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 165; DB 2;
Pred. No. 3.42e-09;
31; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Samejima,
                                                                                                                                                                                                                                                                                        30-Jun-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sakurai, N.; Kaji, H.;
ma, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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74-156
SUMMARY
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                                                                                                            Query Match
Best Local
                                                                                               Matches
176 KRIKPGYLEATVDWFRRYKVPDGK 199
                       113 EDLPOHKLKEIAHFFERYKDLOGK 136
                                               116
                                                                     56 DGDPLDILVITTNPPFPGCVIDTRVIGYLNMVDSGEEDAKLIGVPVEDP---RFDEVRSI 112
                                              DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV 175
                                                                                                         7.2%;
Similarity 33.3%;
                                                                                               28;
                                                                                                                                               Conservative
                                                                                               18;
                                                                                                         Score 154; DB 2;
Pred. No. 1.37e+07;
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Search completed: Thu Sep 17 16:53:28 1998

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. MPsrch_pp Run on: protein - protein database search, using Smith-Waterman algorithm Thu Sep 17 16:53:45 1998; MasPar time 10.59 Seconds 684.218 Million cell updates/sec

Tabular output not generated

Title:

Description: Perfect Score: Sequence:

>US-08-741-437-1 (1-289) from US08741437.pep 2134 1 MSGFSTEERAAPFSLEYRVF......СESACTVPTDVDKWFHHQKN 289

69111 seqs, 25083644 residues

Searched:

Scoring table:

PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 47.360; Variance 80.422; scale 0.589

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB .	ID	Description	Pred. No.
ב	2063	96.7	289	- :	IPYR_BOVIN	INORGANIC PYROPHOSPHAT	0.00e+00
Ŋ	1035	48.5	286	1	IPYR_YEAST		1.47e-213
ω	1019	47.8	286	٢	IPYR_KLULA		1.19e-209
4	939	44.0	288	H	IPYR_SCHPO	INORGANIC PYROPHOSPHAT	3.83e-190
G	812	38.1	310	ب	IPY2_YEAST	INORGANIC PYROPHOSPHAT	2.35e-159
0	658	30.8	114	٢	IPYR_HUMAN	INORGANIC PYROPHOSPHAT	2.02e-122
7	185	8.7	176	<u> </u>	IPYR_THELI	THERMOSTABLE INORGANIC	3.54e-16
8	165	7.7	179	Н	IPYR_THEAC	INORGANIC PYROPHOSPHAT	2.21e-12
9	154	7.2	164	٢	IPYR_BACP3	INORGANIC PYROPHOSPHAT	2.31e-10
10	151	7.1	263	44	IPYR_ARATH	SOLUBLE INORGANIC PYRO	8.03e-10
11	. 149	7.0	173	۳,	IPYR_SULAC	INORGANIC PYROPHOSPHAT	1.83e-09
12	147	6.9	177	H	IPYR_BARBA	INORGANIC PYROPHOSPHAT	4.16e-09
13	147	6.9	211	۳.	IPYR_SOLTU	SOLUBLE INORGANIC PYRO	4.16e-09
14	125	5.9	184	<u></u>	IPYR_MYCPN	INORGANIC PYROPHOSPHAT	2.43e-05
15	122	5.7	176	٢	IPYR_HAEIN	PROBABLE INORGANIC PYR	7.51e-05
16	119	5.6	173	Н	IPYR_HELPY	INORGANIC PYROPHOSPHAT	2.28e-04
17	117	5.5	169	نا	IPYR_SYNY3	INORGANIC PYROPHOSPHAT	4.74e-04
18	118		175	۲	IPYR_ECOLI	INORGANIC PYROPHOSPHAT	3.29e-04
19	117	5.5	184	}_4	IPYR_MYCGE	INORGANIC PYROPHOSPHAT	4.74e-04
20	112	5.2	174	μ	IPYR_THETH	INORGANIC PYROPHOSPHAT	2.86e-03
21	110	5.2	1102	Н	YE20_METJA	HYPOTHETICAL PROTEIN M	5.79e-03
22	107	5.0	814	_	CADF_HUMAN	MUSCLE-CADHERIN PRECUR	1.64e-02
23	104	4.9	365	1	1A03_GORGO	CLASS I HISTOCOMPATIBI	4.56e-02
			4			•	,

25 103 4.8 3124 1 CALC_CHICK COLLAGEM ALPHA ILXII) 26 100 4.7 362 1 1B03_GORGO CLASS I HISTOCOMPATIBI 27 100 4.7 362 1 1B02_GORGO CLASS I HISTOCOMPATIBI 28 100 4.7 362 1 1B02_GORGO CLASS I HISTOCOMPATIBI 29 101 4.7 365 1 1A01_SAGOE CLASS I HISTOCOMPATIBI 30 100 4.7 365 1 1B01_SAGOE CLASS I HISTOCOMPATIBI 31 101 4.7 370 1 1A03_HUMAN HLA CLASS I HISTOCOMPATIBI 31 101 4.7 716 1 ZPZ_FELCA ZONA PELLUCIDA SPERM-B 32 100 4.7 716 1 ZPZ_FELCA ZONA PELLUCIDA SPERM-B 33 101 4.7 788 1 CZY14_NEURC CHLA CLASS I HISTOCOMPA 34 99 4.6 365 1 1A04_PANTR CHLA CLASS I HISTOCOMPA 35 99 4.6 365 1 1A04_PANTR CHLA CLASS I HISTOCOMPA 36 99 4.6 366 1 1C18_HUMAN HLA CLASS I HISTOCOMPA 37 98 4.6 730 1 CADF_MOUSE H-2 CLASS I HISTOCOMPA 38 98 4.6 1750 1 Y832_METJA HYPOTHETICAL PROTEIN M 39 99 4.6 3430 1 POLG_MUT CENOME POLYPROTEIN (CO 40 97 4.5 345 1 HA1F_CHICK CLASS I HISTOCOMPA 41 95 4.5 349 1 GET1_HUMAN HLA CLASS I HISTOCOMPA 42 96 4.5 352 1 HA4F_CHICK CLASS I HISTOCOMPA 43 95 4.5 362 1 1B19_HUMAN HLA CLASS I HISTOCOMPA 44 95 4.5 362 1 1B48_HUMAN HLA CLASS I HISTOCOMPA 45 95 4.5 362 1 1B19_HUMAN HLA CLASS I HISTOCOMPA 46 95 4.5 362 1 1B48_HUMAN HLA CLASS I HISTOCOMPA 47 95 4.5 362 1 1B48_HUMAN HLA CLASS I HISTOCOMPA 48 95 4.5 362 1 1B48_HUMAN HLA CLASS I HISTOCOMPA 49 95 4.5 362 1 1B48_HUMAN HLA CLASS I HISTOCOMPA 40 95 4.5 362 1 1B48_HUMAN HLA CLASS I HISTOCOMPA 41 95 4.5 362 1 1B48_HUMAN HLA CLASS I HISTOCOMPA 42 96 4.5 362 1 1B48_HUMAN HLA CLASS I HISTOCOMPA 43 95 4.5 365 1 YPSC_BACSU HYPOTHETICAL 43.5 KD P	į.																					
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ALIGNMENTS

ALIGNMENTS RESULT ID IPYR BOVIN STANDARD; PRT; 289 AA. AC P37980; DT 011-007-1994 (REL. 30, CREATED) DT 011-007-1994 (REL. 30, LAST SEQUENCE UPDATE) DT 011-007-1994 (REL. 30, LAST SEQUENCE UPDATE) DT 011-007-1997 (REL. 30, LAST ANNOTATION UPDATE) DT 011-007-1997 (REL. 30, LAST ANNOTATION UPDATE) DT 011-007-1997 (REL. 30, LAST ANNOTATION UPDATE) DE HYDROLASE) (PPASE). QC EUTHERIA; ARTIODACTYLA. RN (1) RN (2) RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. RR SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. RR SEQUENCE TO.; MENSELT G.; RN MEDLINE; 93077-59, RA YANG Z., WENSELT G.; RI J. BIOL. CHEM. 267:24641-24647(1992). CC -1- TASSUE SPECIFICITY; HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER CO.; SUBCELLULAR LOCATION: CYTOPLASHIC. CC -1- TSISUE SPECIFICITY; HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER SEGMENTS. CC -1- SUBCELLULAR TO. OTHER PASES. CC -1- SUBCELLULAR TYPE. CC -1- TSISUE SPECIFICITY; HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER SEGMENTS. CC -1- SUBCELLULAR TYPE. CC -1- SUBCELLULAR TYPE. CC -1- TSISUE SPECIFICITY; HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER SEGMENTS. CC -1- SUBCELLULAR TYPE. CC -1- SUBCELLULAR TYPE. CC -1- TSISUE SPECIFICITY; HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER SEGMENTS. CC -1- SUBCELLULAR TYPE. CC -1- TSISUE SPECIFICITY; HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER SEGMENTS. CC -1- SUBCELLULAR TYPE. CC -1- TSISUE SPECIFICITY HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER CC. CC -1- TSISUE SPECIFICITY HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER CC. CC -1- TSISUE SPECIFICITY HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER CC. CC -1- TSISUE SPECIFICITY HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER CC. CC -1- TSISUE SPECIFICITY HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER CC. CC -1- TSISUE SPECIFICITY HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER CC. CC -1- TSISUE SPECIFICITY HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER CC. CC -1- TSIS																													
ALIGNMENTS ALIGNMENTS ADJORD; PRT; 289 AA. 30, CREATED; 30, LAST SEQUENCE UPDATE; 25, LAST ANNOTATION UPDATE) 25, LAST ANNOTATION UPDATE) 26, CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; YITLA. AND PARTIAL SEQUENCE. ATION: CYTOPLASMIC. CITY: HIGHEST LEVELS ARE FOUND IN RETINAL ROD OUTER PLASES. OTHER PASSES. OTHER PASSES. OTHER PASSES. OTHER PASSES. 3. BY SIMILARITY. 32844 MW; ALDSIZC4 CRC32; 96.7%: Score 2063; DB 1; Length 289; 94.8%; Pred. No. 0.00e+00; 10111111111111111111111111111111111	В	å å	oy D		SQ	Z Z	젊딣	DR:				S A	88	ဌ	2 3	7 X	RC	RP .	g C	8	SO	G E		ΡŢ	D.	D :	ð t	RESU	
	DVCEIGSKVCARGEIRVKVLGILAMIDEGETDWKVIAINVEDEDAANVNDINDVKRLKP	ATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDNDPI 	MSSFSSEERAAPFTLEYRVFLKNEKGQYISPFHDIPIYADKEVFHMVVEVPRWSNAKMEI - - - - - - - - - - - -	96.7%; Score 2063; DB 1; Length 289; 94.8%; Pred. No. 0.00e+00; rvative 11; Mismatches 4; Indels 0; Gaps	289 AA; 32844 MW;	E; MAGNESIUM.	HSSP; P00817; 1PYP.	PIR; A45153; A45153.	+!- SIMILARITY: TO OTHER PPASES.	PTM: THE	SEGMENTS.	DE FORM IN DESTRUCT	!- SUBUNIT: HOMODIMER.	- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)0 = 2	m 2	PE;		FROM N.A., AND	EUTHERIA; ARTIODACTYLA.	RDATA; VERTEBRATA; TETRAPODA;	TAURUS	100000	PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE	(REL. 35,	(REL. 30, LAST	(REL. 30.	SIGNBORD, FRI, 203		ALTGUMENTS

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241 241 181

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IPYR_YEAST P00817;

STANDARD;

PRT;

286

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21-JUL-1986 (REL.)1-MAR-1989 (REL.)1-NOV-1997 (REL.

01, CREAT 10, LAST 35, LAST

CREATED)

YDROLASE) (PPASE)

1-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-

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181 GYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKNFAIDIIESTHDYWRALVTKKTDGKGI 240

GYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVTKKTNGKGI

.240

180

SCMNTTVSESPFQCDPDAAKAIVDALPPPCESACTIPTDVDKWFHHQKN 289 SCMNTTLSESPFKCDPDAARAIVDALPPPCESACTVPTDVDKWFHHQKN

289

121 DVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP

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7 7 7 F
   SEQUENCE OF 239-249.
STRAIN=ATCC 38531 / Y.
MEDLINE; 97089742.
NORBECK J., BLOMBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAUR A., BOLES E., MIOSGA ZIMMERMANN F.K.;
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KOLAKOWSKI L.F. JF
SIMILARITY TO E.COLI AND K.LACTIS PPASES.
MEDLINE: 90254161.
LAHTI R., KOLAKOWSKI L.F. JR., HEINONEN J
COOPERMAN B.S.;
                                                                                                                                                                                                                                         ACTIVE SITE.
BOND M.W., CHIU N.Y., COOPERMAN, B.S
BIOCHEMISTRY 19:94-102(1980).
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95203288.
GARRELS J.I., FUTCHER B., KOBAYASHI R.,
VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
ELECTROPHORESIS 15:1466-1486(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE; 78087552
COHEN S.A., STERNI
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ENTIAN K.-D.,
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                                                                                                       HEIKINHEIMO P., LEHTONEN J.,
                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS)
RACTITUMIAN E.G., TERZIAN S.S., VORONO
SMIRNOVA E.A., VAINSTEIN B.K., HOLINE'
DOKL. AKAD. NAUK SSSR 258:1481(1981).
                                                                                                                                                                                                                                                                                                 ORBECK J., BLOMBERG A.;
PEMS MICROBIOL, LETT. 137:1-8(1996).
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                                                                            STRUCTURE 4:1491-1508(1996)
                                                                                                                        EDLINE; 97148342
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                                                                                                                                     -RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., SCHLOESSER M., COOPERMAN B.S.; 16:10441-10452(1988).
                                                                                                                                                                                                                                                                                                                                                Y41;
                                                                                                                                                                                3.0 ANGSTROMS).
N S.S., VORONOV
N B.K., HOHNE W
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T., S
                                                                                                        BAYKOV A.,
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                                                                                                                                                                                  VORONOVA A.A.,
HOHNE W.E., HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEMIASCOMYCETES
                  HEINONEN J.,
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                                                                                                        LAHTI
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                                                                                                                                                                                  A., KURANOVA I.P., HANSEN G.;
                  VIHINEN
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                                                                                                            COOPERMAN
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                    POHJANOKSA K.,
                                                                                                            B.S.,
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FSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIYADKD--VFHMVVEVPRWSNAKMEIA 61

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Mismatches

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EMBL; Z35880; G53620
PIR; S45864; PWBY.
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-!- SUBCELLULAR LOCATION:
-!- SIMILARITY: TO OTHER
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Similarity
151; Conser
                                                                                                                                                                                                                                                                                                                                                                                                       PS00387; FE
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                                  286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G536206;
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        48.5%;
53.0%;
                                  32184 MW;
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D -> N (IN REF. 3).
MISSING (IN REF. 3).
E -> Q (IN REF. 3).
Q -> E (IN REF. 3).
Q -> D (IN REF. 3).
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Score 1035;
Pred. No. 1.
60; Mismatc
                                  0318010F CRC32;
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         .47e-21
                  DB 1;
                 Length 286;
 Indels 10;
Gaps
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Best Local :
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01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE).
                                                                                                                                                                                                                                                                                       ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPYR_KLULA
P13998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 89189093.
STARK M.J.R., MILNER J.S.;
YEAST 5:35-50(1989).
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOCHIM. BIOPHYS. ACTA 1038:338-345(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 90254161.
LAHTI R., KOLAKOWSKI L.F. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY TO E.COLI AND YEAST PPASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; FUNGI; ASCOMYCOTINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COOPERMAN B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLUYVEROMYCES LACTIS (YEAST)
                179
                                           121
                                                                                                                                                                                                                                                                                                                  NIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                 :- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 
!- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVI!- SUBUNIT: HOMODIMER.
                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
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                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: CYTOPLASMIC SIMILARITY: TO OTHER PPASES.
                                                       DVLEIGEQVAYTGQVKQVKVLGVMALLDEGETDWKYIAIDINDPLAPKLNDIEDVEKHL- 178
                                                                                                              SYTTRQVGAKNSLDYKYYIEKD-GKPISAFHDIPLYADEANGIFNMVVEIPRWTNAKLEI
                                                                                                                                                                                                                                                                                                                                                                            S07894; PWVKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLTNVTLPDTP-TY-SKAA-S--DAIPPASLKADAPIDKSIDKWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLEIGETIAYTGQVKQVKALGIMALLDEGETDWKVIAIDINDPLAPKLNDIEDVEKYFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEETLNPIIQDTKKGKLRFVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPID
                                        DVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV-KRLK
                                                                                                 ATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDNDPI
                                                                                                                                                        GFSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIYADK-D-VFHMVVEVPRWSNAKMEI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLEATYDWFRRYKYPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALYT-KKTNGKGI
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           PGLLRATNEWFRIYKIPDGKPENQFAFSGEAKNKKYTLDVIRECNEAWKKLISGKSADAK 238
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                                                                                                                                                                                                                                                                                                                                             P00817; 1PYP.
FE; PS00387; PPASE;
                                                                                                                                                                                                                                                                                                                                                                                        X14230; G2903;
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                SOUSE, MAGNESIUM.
286 AA;
                                                                                                                                                                                                               47.8%;
llarity 51.4%;
Conservative
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                                                                                                                                                                                                                                                                       56 F
78 I
32034 MW;
                                                                                                                                                                                                               Score 1019; DB 1;
Pred. No. 1.19e-209;
66; Mismatches 63;
                                                                                                                                                                                                                                                                  BY SIMILARITY.
PROBABLE.
INORGANIC PYROPHOSPHATE (BY SIMILARITY).
748339D5 CRC32;
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[1]
SEQUENCE FROM N.A.
MEDLINE; 91016938.
MEDLINE; 91016938.
MEDLINE; 91016938.
18:5888-5888(1990).
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P19117;
01-NOV-1990
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SEQUENCE
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01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-CCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHINEN M., LUNDIN M., BALTSCHEFFSKY H.;
BIOCHEM. BIOPHYS. RES. COMMUN. 186:122-128(1992).
-I- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
-I- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
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EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               !- SUBCELLULAR LOCATION: CYTOPL !- SIMILARITY: TO OTHER PPASES. MBL; X54301; G5014; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATION. MAGNESIUM CONFERS SUBUNIT: HOMODIMER.
                                                                                                         G-ISCMNTTLSESPFKCDPDAARAIVDALPPPCESACTVPTDVDKWF
                                                                                                                                                                                SDFSLVNVSVTGSVAN-DPSVSSTIPPA-QEL-APA-PVDPSVHKWF
                                                                                                                                                                                                                                                                                          MPGLIRATNEWFRIYKIPDGKPENSFAFSGECKNRKYAEEVVRECNEAWERLITGKTDAK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDVCEIGEARGYT-GOVKQVKVLGVMALLDEGETDWKVIVIDVNDPLAPKLNDIEDVERH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRETATION OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                    KPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVTKKTNGK 238
                                                                                                                                                                                                                                                                                                                                                                                            IDVCEIG-SKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITKEATLNPIKQDTKKGKLRFVRNCFPHHGYIWNYGAFPQTYEDPNVVHPETKAKGDSDP 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92337585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.0%;
larity 48.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
79
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32336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 939; DB 1; I
Pred. No. 3.83e-190;
66; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.6.1.1) (PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEED9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIGHEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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IPY2_YEAST: ST: P28239; 01-DEC-1992 (REL.

STANDARD;

PRT;

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Best Local Similarity
Matches 113; Consei
                       IPYR_HUMAN STANDARD; PRT; 114 AA. Q15181; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                         ACT_S
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M81880; G172223; -. EMBL; Z49260; G809090; -. PIR; A40867; A40867.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=W303-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SACCHAROMYCES CEREVISIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PYROPHOSPHATE PHOSPHO-HYDROLASE)
IPP2 OR PPA2 OR YMR267W OR YM8156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992
01-OCT-1996
  PP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
              HYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "UNDIN M.,
                                                                                                                                       178
                                                                                                                                                              214
                                                                                                                                                                                       118
                                                                                                                                                                                                                154
                                                                                                                                                                                                                                                                                                             34 FSTIQQGSKYTLGFKKYLTLLNGEVGSFFHDVPLDLNEHEKTVNMIVEVPRWTTGKFEIS 93
                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPH
PYROPHOSPHATASE THAT IS ESSENTIAL FOR MITCCHONDRIAL FUNCT
SUBUNIT: HOMODIMER THAT BEXINDS MONCOVALENTLY TO A PROTEIN
IN THE INNER MITOCHONDRIAL MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: MITOCHONDRIAL SIMILARITY: TO OTHER PPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INEN M., LUNDIN M., BALTSCHEFFSKY H.;
CHEM. BIOPHYS. RES. COMMUN. 186:122-128(1992).
FUNCTION: INVOLVED IN ENERGY PRODUCTION. ITS
                                                                                                                                                                                                                                                                                                                                                                                                         SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STIMULATED BY UNCOUPLERS OF ATP SYNTHESIS.
                                                                                                                                                                                                                                                     KELFENPIVQDTKNGKLRFVNNIFPYHGYIHNYGAIPQTWEDPTIEHKLGKCDVALKGDN 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                        L0001469; PPA2
[TE; PS00387; P]
                                                                                                                                       LKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVT
                                                                                                                                                              YFPGILDTTREWFRKYKVPAGKPLNSFAFHEQYQNSNKTIQTIKKCHNSWKNLIS
                                                                                                                                                                                       DPLDCCEIGSDVLEMGSIKKVKVLGSLALIDDGELDWKVIVIDVNDPLSSKIDDLEKIEE
                                                                                                                                                                                                                                         TKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGC-C---GDN
                                                                                                                                                                                                                                                                                          FSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPI-YADKD-VFHMVVEVPRWSNAKMEIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S288C / AB972;
CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A.;
ED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91286226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYROPHOSPHATASE,
                                                                                                                                                                                                                                                                                                                                                                                         31 3
89
310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BALTSCHEFFSKY H., RONNE H. 
HEM. 266:12168-12172(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL.
              (PPASE)
                                                                                                                                                                                                                                                                                                                                         38.1%;
larity 48.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASCOMYCOTINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                  310
                                                                                                                                                                                                                                                                                                                                                                                         89
.35572 MW;
              (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAST
LAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRIAL PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                         Score 812; DB 1; I
Pred. No. 2.35e-159;
51; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRION (POTENTIAL) INORGANIC PYROPHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                           C1DC143B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PPASE).
                                                                                                                                                                                                                                                                                                                                           65;
                                                                                                                                                                                                                                                                                                                                                                  Length 310,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EC 3.6.1.1)
                            PHOSPHO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SI
                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEX
                                                                                                                                        232
                                                                                                                                                                268
                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local
                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 2.030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
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EUTHERIA; F
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
LACROIX J., VIGNERON
SUBMITTED (MAR-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
                                                                                                                                     HYDROLASE; MAGNESIUM.
ACT_SITE 30 3
                                                                                                                                                                                                                                                                                                                                                                        IPYR_THELI
P77992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00387; PPASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: CYTOPLASMIC
-!- SIMILARITY: TO OTHER PPASES.
                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                          01-NOV-1997
01-NOV-1997
                                                                                                                                                         -!- SIMILARITY: TO OTHER PP
EMBL; U49440; G1518483; -.
PROSITE; PS00387; PPASE; 1.
                                                                                                                                                                                                              LENNOX T.L., SEARS L.E., MORAN L.S., SLATKO B.E.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (SEP-17917Y: PYROPHOSPHATE + H(2)O = 2 PHOSPHATE.
-!- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                      THERMOCOCCUS LI
                                                                                                                                                                                                                                                                                                                     PHOSPHO-HYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                        HERMOSTABLE
                      126
  176
                                         116
                                                                                                                                                                                         !- SUBCELLULAR LOCATION:
                                                                                                                                                                                                             - CATALYTIC ACTIVITY: PYROPHOSE
- COFACTOR: REQUIRES MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                             66
                                                                                                                                                                                                   - SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                              -NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROIX J., VIGNERON M., KEDINGER C.,
MITTED (MAR-1995) TO EMBL/GENBARE + H(2)O -
CATALYIK ACTIVITY: PXOPHOSPHATE + H(2)O -
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                       DDDPFDIMVIMREPTYPGVLIEARPIGLFKMIDSGDKDYKVLAVPVEDPYFNDWKDISDV
                   -P-KA-FLDEIAHFFQRYKELQGK 146
   KRLKPGYLEATVDWFRRYKVPDGK
                                         DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z48605; G727225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
83; Conser
                                                                                 h 8.7%;
Similarity 36.9%;
31; Conservative
                                                                                                                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGNESIUM.
                                                                                                                           176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 AA;
                                                                                                                                                                                                                                                                                                                                         (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
                                                                                                                                                                                                                                                                                      LITORALIS.
IA; CRENARCHAEOTA;
                                                                                                                                                                                                                                                                                                                             REL. 35, CREATED)
REL. 35, LAST SEQUENCE UPDATE)
REL. 35, LAST ANNOTATION UPDATE)
INORGANIC PYROPHOSPHATASE (EC 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13045 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114
                                                                                                                                                                              OTHER PPASES
                                                                                                                                                                                                                                                                                                                     (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHORDATA;
                                                                                                                           20659 MW;
                                                                                                                                         30
                                                                                                                                                                                          CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 658; DB 1; L
Pred. No. 2.02e-122;
21; Mismatches 10;
                                                                                  Score
Pred.
20; M
                                                                                                                            BY SIMILARITY.
; 3DB64F1F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERTEBRATA; TETRAPODA;
   199
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42DF6303 CRC32;
                                                                                                                                                                                                                                                                                       THERMOPROTEALES; THERMOCOCCACEAE.
                                                                                  e 185; DB 1; Le
. No. 3.54e-16;
Mismatches 30;
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                                                                                               3.6.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 114;
                                                                                                      Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                               (PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                             ICHIBA T., TAKENAKA O., SAMEJIMA T., HACHIMORI A.;

J. BICCHEM. 108:572-578 (1990).

-I- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.

-I- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL

CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY.

-I- SUBUNIT: HOMOTRIMER. IN PRESENCE OF DIVALENT CATIONS THE TRIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 93011147.
RICHTER O.-M.H., S
EUR. J. BIOCHEM. 2
                                             AGGREGATE TO FORM A HEXAMER.
-!- SUBCELLULAR LOCATION: CYTOPI
-!- SIMILARITY: TO OTHER PPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RICHTER O.-M.H., SCHAEFER G.;
EUR. J. BIOCHEM. 209:343-349(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-DSM 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THERMOPLASMA ACIDOPHILUM.
ARCHAEBACTERIA; EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (REL.
01-FEB-1995 (REL.
                                                                                                                                                                                          PROKARYOTA;
                                                                                                                                                                                                     BACILLUS PS3
                                                                                                                                                                                                                             HYDROLASE) (PPASE).
                                                                                                                                                                                                                                        01-FEB-1991
01-NOV-1997
INORGANIC PY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROLASE; MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-22, MEDLINE; 93011146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INORGANIC PYROPHOSPHATASE
                                                                                                                                                      EDLINE; 91154162
                                                                                                                                                                                                                                                                                               PYR_BACP3
                                                                                                                                                                                                                                                                                                                                                176
                                                                                                                                                                                                                                                                                                                                                                   124 KDVNAHLLDEIANFFSTYKILEKKETKVLGWEGKEAALKEIEVSI
                                                                                                                                                                                                                                                                                                                                                                                               116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [PYR_THEAC
                                                                                                                                                                   EQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                    67 DGDPMDVMVLISQPTFPGAIMKVRPIGMMKMVDQGETDNKILAVFDKDPNVS-Y--IKDL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IR; S29313; S29313.
                                                                                                                                                                                                                                                                          -FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO OTHER PPASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC
                                                                                                                                                                                                                                                                                                                                              KRIKPGYLEATVDWFRRYKVPDGKPENEFAFNA-EFKDKDFAIDI
                                                                                                                                                                                                                                                                                                                                                                                            DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P17288; 1EIP
                         P17288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                    991 (REL. 17, LAST
997 (REL. 35, LAST
C PYROPHOSPHATASE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 AA;
                                                                                                                                                                                          FIRMICUTES;
                                   JX0135.
                                                                                                                                                                                                     (THERMOPHILIC
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G48082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVITY: PYROPHOSPHATE + AR LOCATION: CYTOPLASMIC.
                        1EIP.
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHAEFER G.;
209:351-355(1992).
                                                                                                                                                                                                                                   17, CREATED)
17, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
SPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
            PPASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31
20465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.78;
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LAST
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                                                                                                                                                                                        IC BACTERIUM PS-3)
                                                          CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 165; DB 1; Lengard No. 2.21e-12; Pred. No. 2.21e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE UPDATE)
ANNOTATION UPDATE)
(EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
; CC7397F6 CRC32;
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                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                219
                                                                                 THE TRIMERS
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                                                                                                                                                                                          BACILLACEAE
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Matches
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SEQUENCE
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01-MAR-1992
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X57545; G16348;
PIR; S13379; S13379.
HSSP; P17288; 1EIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIEBER J.J., SIGNER E.R.;
PLANT MOL. BIOL. 16:345-348(1991).
-i- CATALYTIC ACTIVITY: DEPENDENT ON MG2+
-i- COFACTOR: ACTIVITY DEPENDENT ON MG2+
                                                                                               01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
                                                                                                                                                             P50308;
STRAIN-DSM 639;
            SEQUENCE FROM N.A.,
                                        ARCHAEBACTERIA;
                                                         SULFOLOBUS ACIDOCALDARIUS
                                                                                                                                                                              IPYR
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARABIDOPSIS THALIANA (MOUSE-EAR EUKARYOTA; PLANTA; EMBRYOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPYR_ARATH P21216;
                                                                                     HYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. COLUMBIA; MEDLINE; 91370878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOLUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAPPARALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
                                                                                                                                                                                                                                         174 DV
                                                                                                                                                                                                                                                                  162 EL
                                                                                                                                                                                                                                                                                                114 CGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIN 173
                                                                                                                                                                                                                                                                                                                          102 CEDSDPMDVLVLMQEPVLTGSFLRARAIGLMPMIDQGEKDDKIIAVCADDPEFRHYRDIK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 KRLKPGYLEATVDWFRRYKVPDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :- SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 DGDPLDILVITTNPPFPGCVIDTRVIGYLNMVDSGEEDAKLIGVPVEDP---RFDEVRSI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                              SULAC
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                                                                                                                                                                                                                                                                    , 163
                                                                                                                                                                                                                                                                                                                                                          Similarity
23; Conser
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28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    992 (REL. 21, CREATED)
1992 (REL. 21, LAST SNOUENCE UP
1997 (REL. 35, LAST ANOTATION
INORGANIC PYROPHOSPHATASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAGNESIUM.
                                                                                       (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     263 AA;
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larity 37.1%;
Conservative
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                                                                                                                                                                             STANDARD;
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                                        CRENARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPASE; '1.
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33.3%;
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18792
            PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                     29712 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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            SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                        Score 151; DB 1;
Pred. No. 8.03e-10;
18; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 154; DB 1;
Pred. No. 2.31e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
; FF88D7C4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199
                                                                                                                                                                             PRT;
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                                        SULFOLOBALES
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                                                                                                                                                                             173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 AA.
          AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
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2+ (BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                   CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                    Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PYROPHOSPHATE PHOSPHO
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                                                                                                                                                                                                                                                                                                                                                          Indels
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2 ORTHOPHOSPHATE

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Best Local
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Best Local
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MEYER W., MOLL R., KATH T., SCHAFER G.;

ARCH. BIOCHEM. BIOPHYS. 319:149-156(1995).

-i- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)0 = 2

-i- COFACTOR: ABSOLUTE REQUIREMENT FOR MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P51064;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROLASE; MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
INDRGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
                                                                                                                                                                                                                                                                                                                         STRALM=NCOO;
MITCHELL S.J., MINNICK M.F.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-i- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
-i- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL
-i- COFACTOR: THIS ENZYME REQUIRES THE HIGHEST ACTIVITY. BINDS 4 DIVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           BARTONELLA BACILLIFORMIS. PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYDROLASE)
 IPYR_SOLTU
Q43187;
                                                                                                                                                                                                              HYDROLASE; MAGNESIUM.
ACT_SITE 30
SEQUENCE 177 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-KC583;
                                                                                                                                                                                                                                                                                                                                                                                                                                BARTONELLACEAE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [PYR_BARBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                              116
                                                              176
                                                                                     125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: TO OTHER PPASES.
L; x81842; G886704; -.
SITE; PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION:
                                                                                                                                      66
                                                                                                                                                                                                                                                                           CATION. MAGNESIUM CONFERS THE HIGHEST CATIONS PER SUBUNIT (BY SIMILARITY).
SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: TO OTHER PPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNDPIDVCEIGS-KVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIND 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGDPLDVLVITNYQLXP-GSVIEVRPIGILYMKDEEGEDAKIVAVPKDKTDPS-FSNIKD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDLPQATKNKIVHFFEHYKELEPGK 145
                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKRLKPGYLEATVDWFRRYKVPD-GK 199
                                                                                                                                  DSDPIDVLVCNTRPLIPGCVINVRPIGALIMEDDGGKDEKIIAVPTPKL-TQQYIGIHDY 124
                                                          KRLKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKAL
                                                                          TDLTENILKKIEHFFKHYK--DLEAGK-WAKIEGWRDKNFARELIQQAIERAKAI 176
                                                                                                             L46591; G940255; -.
re; PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 7.0%;
Similarity 33.7%;
29; Conservative
                                                                                                                                                              h 6.9%;
Similarity 30.4%;
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
19381 MW;
                                                                                                                                                                                                                 30 I
20064 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                               SCOTOBACTERIA; RICKETTSIAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 149; DB 1;
Pred. No. 1.83e-09;
22; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                Score 147; DB 1;
Pred. No. 4.16e-09
23; Mismatches 5
                                                                                                                                                                                                                                ВУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4F4E97B3
              PRT;
                                                                                                                                                                                                                     31852443
                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
                  211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC32;
                                                                                                                                                                                                                    CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                          Length 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RICKETTSIALES
                                                                                                                                                                                                                                                                                                                                       METAL
DIVALENT
                                                                                                                                                                     4;
                                                                    230
                                                                                                                                                                      Gaps
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Best Local S
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Query Match
Best Local S
Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPA.
SOLANUM TUBEROSUM (POTATO).
EUKARYOTA; PLANTA; EMBRYOPHYTA;
SOLANALES; SOLANACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DU JARDIN P., ROJAS-BELTRAN J., GEBHARDT
PLANT PHYSIOL. 109:853-860(1995).
PLANT PHYSIOL. 109:853-860(1995).
-I- COFACTOR: ACTIVITY DEPENDENT ON MG2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYDROLASE) (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYDROLASE; MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                        IPYR_MYCPN P75250;
                                           HYDROLASE;
                                                                                        MYCOPLASMA PNEUMONIAE.
PROKARYOTA; TENERICUTES;
                                                                                                                                                                                                                                                           HYDROLASE)
                                                                                                                                                                                                                                                                             01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                              01-NOV-1997
                                                                                                                                                                                STRAIN-ATCC 29342
MEDLINE; 97105885
                                                             -!- SIMILARITY: TO OTHER PPASES.
EMBL; AE000029; G1673987; -.
PROSITE; PS00387; PPASE; 1.
                                                                                                                                                                                                                      MYCOPLASMATACEAE.
                                                                                                                                                                                                                                                                     INORGANIC
                                                                                                                                                                                                                                                                                                                                                       174
                                                                                                                                                                                                                                                                                                                                                                                            114
                                  SEQUENCE
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         154
                                                                                                                                                                      HIMMELREICH R., HILBERT H.,
                                                                                                                                                             ERRMANN R
                                                                                                                                                                                                                                                                                                                                                                                                               95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: CYTOPI
SIMILARITY: TO OTHER PPASES
                                                                                                                                                                                                                                                                                                                                                                                           CGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIN
                                                                                                                                                                                                                                                                                                                                                                                                             CEDNDPMDVLVLMQEPVLPGCFLRARAIGLMPMIDQGEKDDKIIAVCADDPEYRHYTDI-
                                                                                                                                                                                                                                                                                                                                                      DVKRLKPGYLEATVDWFRRYKVPDGK 199
                                                                                                                                                                                                                                                                                                                                                                       --KOLPPHRLAEIRRFFEDYKKNENK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z36894; G534916; -.
NE; PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
32; Conser
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        Similarity
                                                                                                                                                                                                                                                                     PYROPHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA;
                                                                                                                                                                                                                                                            (PPASE).
                                                                                                                                                                                                                                                                              (REL.
                                    184
                                                     MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                    A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35, CREATED)
35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
PYROPHOSPHATASE (EC 3.6.1.1)
                                                                                                                                                                                                                                                                    35, CARATED)
35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
35, LAST ANNOTATION UPDATE
35PHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 E
24261 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            6.9%;
37:2%;
          5.9%;
28.6%;
                                                                                                                                                                                           M129;
                                    21369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC.
                                                                                                                                                                                                                                MOLLICUTES; MYCOPLASMA;
                                     WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
16; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY 8F8FC92C CRC
 Score
Pred.
22; M
                                                                                                                                                                         PLAGENS H.,
                                              ву
                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEBHARDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANGIOSPERMAE; DICOTYLEDONEAE;
                                       D5F880FD
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                              SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                            147; DB 1;
No. 4.16e-09;
  Mismatches
           125; DB 1;
No. 2.43e-05;
                                                                                                                                                                                                                                                                                                                     184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H(2)0
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                                     CRC32;
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ESENCE OF DIVALENT METAL
ACTIVITY. BINDS 4 DIVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BRASSEUR R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PYROPHOSPHATE PHOSPHO-
    20;
                                                                                                                                                                          Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                     Length 184;
                                                                                                                                                                                                                                   MYCOPLASMATALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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    Indels
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     Gaps
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18;

Conservative

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Search completed: Thu Sep 17 16:54:43 1998 Job time: 58 secs.
                                                                                                                                                                                                                                                                                  Query Match 5.7%;
Best Local Similarity 29.6%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCIENCE 269:496-512(1995).

SCIENCE 269:496-512(1995).

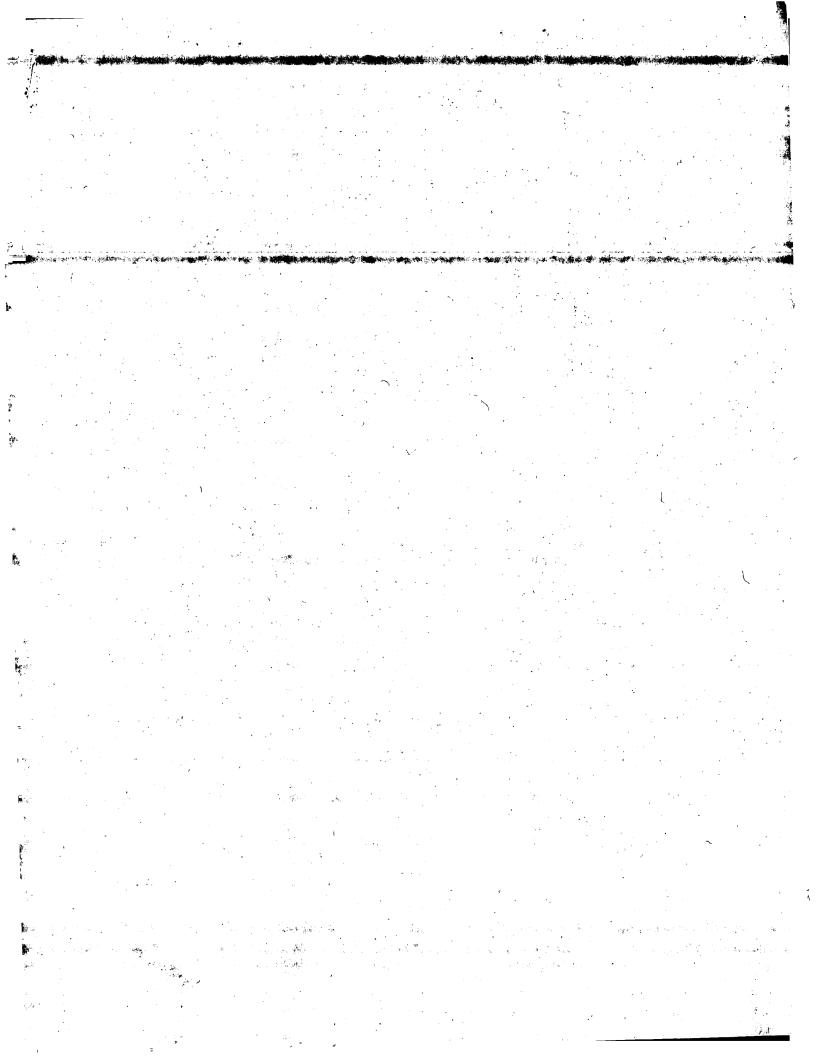
CATALTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.

COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL

CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY. BINDS 4 DIVALENT

CATIONS PER SUBUNIT (BY SIMILARITY).

CATIONS PER SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F. KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M. MCKERNEY K., SUTTON G., EITZHUGH W., FIELDS C.A., GOCAYME J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., WEIDMAN J.F., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S. M., GRNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPYR_HAEIN P44529;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (REL.
01-NOV-1995 (REL.
01-NOV-1995 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                           HYDROLASE; MAGNESIUM.
ACT_SITE 31 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 YKV 195
                                                                                          175 VKRLKPGYLEATVDW-FRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  !- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 ---L-PANLIKQIEFHFNNYKALK-KPGST-KV-THWGDVEEAKEVIRESIKRWN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   !- SIMILARITY: TO OTHER PPASES.
MBL; U32698; G1573079; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEMOPHILUS INFLUENZAE.
ROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROBABLE INORGANIC PYROPHOS HOSPHO-HYDROLASE) (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 YKL 131
                                                                                                                                                                                        116 DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAAN-YNDIND 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASTEURELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA OR HI0124.
                                                                                                                                                                                                                                 67 DGDELDVLLITRQPLATGVFLEAKVIGVMKFVDDGEVDDKIVCVPADDRDTGNAYNSLAD 126
                                                                                                                                                                                                                                                                                                                                                                                31 31 E
176 AA; 19725 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32, CREATED)
32, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
C PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC.
                                                                                                                                                                                                                                                                                  Score 122; DB 1;
Pred. No. 7.51e-05;
26; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
; CE8BDD6F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOUGHERTY B.A., MERRICK J.M.,
                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                                                               Length 176;
                                                                                                                                                                                                                                                                                     Indels
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993:1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated Thu Sep 17 16:55:00 1998; MasPar time 18.79 Seconds 647.612 Million cell updates/sec

Description: Perfect Score: >US-08-741-437-1 (1-289) from US08741437.pep 2134

Sequence: 1 MSGFSTEERAAPFSLEYRVF......CESACTVPTDVDKWFHHQKN 289

Scoring table: PAM 150 Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate 13:sp_unclassified

Statistics: Mean 46.257; Variance 82.300; scale 0.562

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	. Re
20 20 20 20 20 20 20 20 20 20 20 20 20 2	Result No.
1005 864 154 143 123 123 123 117 100 100 107 107 107 107 107 107 107	Score
4477 400 400 400 400 400 400 400 400 400	Query Match
285 285 286 116 1176 1176 215 214 214 214 214 357 357 357 357 357 357 357 357 357 357	Length
	DB C
013505 013505 013505 015724 023979 026363 049071 022537 034955 034955 034955 030444 030914 030914 030914 030914 030914 030914 030916 030916 030916 030916 030916 030916 030916 030916 030916 030916	ID
INORGANIC PYROPHOSPHAT INORGANIC PYROPHOSPHATASE (FRAGM SOLUBLE INORGANIC PYROPHOSPHAT MHC CLASS I ATBECURSOR MHC CLASS I ANTIGEN MHC CLASS I HISTOCOMPA MHC CLASS I ANTIGEN MHC CLASS I ANTIGEN MHC TYPE I ANTIGEN MHC TYPE I ANTIGEN (FR MHC TYPE I ANTIGEN (FR MHC CLASS I CAJA-G*05	Description
2.86e-197 2.86e-194 8.72e-164 8.76e-08 4.35e-05 1.30e-08 1.12e-03 1.12e-03 1.12e-03 1.78e-02 1.78e-02 3.49e-02 3.49e-02 3.49e-02 9.43e-02 9.43e-02 9.43e-02 1.81e-01 1.31e-01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
99	99	99	98	99			98	99	99	99	99	101	101	101	101	100	100	100	101	100	101	101	103	103
4.6	4.6	4.6	4.6	4.6	4	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7		4.8	4.8
366	366	366	358	357	356	347	246	181	91	91	91	3063	365	363	363	354	354	344	294	181	166	166	1462	362
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Q29864	Q31605	Q29991	Q30291	Q30917	Q30171	Q29505	Q29945	019505	019635	P79617	Q31189	Q99715	019756	Q29840	019642	Q95513	Q95514	P79602	Q30714	019354	Q95516	Q95518	034313	P79523
CHAIN	ALPHA CHAIN OF MHC CLA	HLA CLASS I HEAVY CHAI	1 PR	MHC CLASS I A (FRAGMEN	LYMPHOCYTE ANTIGEN.	GALACTOSIDE 2-L-FUCOSY	MHC CLASS I HLA-A CELL	HLA-CW6 (FRAGMENT).	MHC CLASS I ANTIGEN HL	MHC CLASS I HLA-C (FRA	MHC CLASS I H2-K-ALPHA	COLLAGEN TYPE XII ALPH	MHC CLASS I HLA-A.	HLA-A*03	MHC CLASS I ANTIGEN HL	HISTOCOMPATIBILITY ANT	HISTOCOMPATIBILITY ANT	MATURE ALPHA CHAIN OF	MHC CLASS I ANTIGEN MA	MHC CLASS I A ANTIGEN	HISTOCOMPATIBILITY ANT	HISTOCOMPATIBILITY ANT	YFKN PROTEIN.	MHC CLASS I HISTOCOMPA
4.74e-01	4.74e-01	4.74e-01	6.49e-01	4.74e-01	6.49e-01	4.74e-01	6.49e-01	4.74e-01	4.74e-01	4.74e-01	4.74e-01	2.50e-01	2.50e-01	2.50e-01	2.50e-01	3.45e-01	3.45e-01	3.45e-01	· 2.50e-01	3.45e-01	2.50e-01		.31e	1.31e-01

ALIGNMENTS

Db 70 T	Db 11 Y Oy 4 F	Query Match Best Local Matches 1	HYPOTI SEQUE		RA THIERRY-MIE			RA CRAXTO	RA WILSON		RN [2]		RP SEQUENCE	OC EUKARY			DT 01-JAN-1998	DT 01-NOV-1996	AC Q18680;
TKEPFSPIKQDEKKGVARFVHN : :: TKDPLNPIKQDVKKGKLRYVAN	<pre>ZEAVERGSLYSLDYRVYIKGPQ : : :::: : :: FSTEERAAPFSLEYRVFLKNEK</pre>	tch 52.4%; al Similarity 53.2%; 150; Conservative	EMBL; 200882; E348322; HYPOTHETICAL PROTEIN. SEQUENCE 292 AA; 32363 MW;	WATSON A., WEINSTOCK L., WINATURE 368:32-38(1994).	ON N., SMITH A., SONNH	PARSONS J., PERCY C., RIFKE	M., KERSHAW J., KIRST	DN M., DEAR S., DU Z.,	WILSON R., AINSCOUGH R., AN BONFIELD J., BURTON J., CON	SEQUENCE FROM N.A. MEDLINE; 94150718.	(GWN-1330) IO	173N-1996) mo	NCE FROM N.A.	EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA;	1	L PROTEIN C4	4-1998 (TREMBLREL, 05,	(TREMBLREL.);
TKEPFSPIKQDEKKGVARFVHNIFPHKGYIWNYGALPQTWEDPNHVVPDTGAKGDNDPID : ::	YEAVERGSLYSLDYRVYIKGPQG-IVSDWHDIPLFANKDKRVYNMIVEIPRWTNAKMEMA : : :: : : : : : :: : :: : :	Score 1119; DB 3; Length 292; Pred. No. 6.23e-224; 65; Mismatches 60; Indels	W; A31DC923 CRC32;	WILKINSON-SPROAT J., WOHLDMAN P.;	THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON	RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN	EN J., LAISTER N., LATREIL	CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M. BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,		EMBL/GENERNA/DUBO DAIA BANAS.	2		ATES; NEMATODA; SECERNENTEA;	•	Ç	LAST SEQUENCE UPDATE:		2 / 2 / 2 / 2 / 2 / 2 / 2 / 2 / 2 / 2 /
TGAKGDNDPID 129 TGCCGDNDPID 121	(PRWINAKMEMA 69 	n 292; els 7; Gaps 6;			DN J.,	D., SHOWNKEEN R.,	E P.,	JOHNSTON I.	J., COULSON A.,					A; RHABDITIDA.					

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Query Match
-- rocal Similarity Conser
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013505;
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01-JAN-1998 (TREMBLREL 05,
01-JAN-1998 (TREMBLREL 05,
INORGANIC PYROPHOSPHATASE (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COSANO I., ALVAREZ.P., MOI
SUBMITTED (NOV-1997) TO EX
EMBL; AJ001000; E1180018;
HYDROLASE; PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 VCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 VIEVGSKVAGRGAVLQVKVLGTLALIDEGETDWKLVAIDVNDENADKLNDIDDVEKVYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PICHIA PASTORIS (YEAST).
PLASMID PRS316-GAL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 LLAASVEWFRNYKIPAGKPANEFAFNGEFKNREYAEKVIDETNEYWKTLI-KEANP-SLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=NRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UKARYOTA;
                                                                                                                           P87118
P87118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A
BADCOCK
           SEQUENCE FROM N.A. STRAIN-972H-;
                                             EUKARYOTA; FUNGI;
                                                        SCHIZOSACCHAROMYCES POMBE
                                                                                           01-JUL-1997 (TREMBLREL: 04, CREATED)
01-JUL-1997 (TREMBLREL: 04; LAST SEQUENCE UI
01-JUL-1997 (TREMBLREL: 04, LAST ANNOTATION
                                                                                                                                                                                                                                179
                                                                                                                                                                                                                                                       178
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                                                                                                                                                                                                                                                                                                 119 PLDVCEIGERSYT-GQVKQVKVLGVMALLDEGETDWKVIVIDINDPLAPKLNDIEDVEKH 177
                                                                                                                                                                                 239 GISCMNTTLSESPFKCDPDAARAIVDALPPPCESACTVPTDVDKWF 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CMNTTLSESPFKCDPDAARAIVDALPPPCESACTVPTDVDKW
                                                                                                                                                                                                                                                                                                                                                                        MS-YSTRQIGAANTLENRVFIEKD-GQVVSPFHDIPLYADESKKVLNMVVEVPRWTNAKL
                                                                                                                                                                                                                                KPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVTKKTNGK 238
                                                                                                                                                                                                                                            PIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRL
                                                                                                                                                                                                                                                                                                                        EIATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDND 118
                                                                                                                                                                                                      EIDLTNTTLOSTP-SFSPSATSAVPTA-SPA-APA-KIDQSIDKWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 AA;
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  CHURCHER C.M.;
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                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   47.1%;
52.4%;
                                             ASCOMYCOTINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32068 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLINA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PYROPHOSPHATE PHOSPHO-HYDROLASE) (EC
                                                (FISSION YEAST).
OTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1005; DB 1;
Pred. No. 2.86e-197;
56; Mismatches 71;
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                                                                                              SEQUENCE UPDATE)
ANNOTATION UPDATE
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DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Query Match
Best Local Simi
Matches 122;
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Best Local S
Matches 2
                                                                                                                                                                                                                                                                                 SATOH T., ISHII K., KOYAMA
IRIE M., SAMEJIMA T.;
SUBMITTED (MAX-1997) TO EMB
EMBL; ABB03087; D1020624;
NON_TER 164 164
SEQUENCE 164 AA; 18796 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (MAY-1997) TO E EMBL; Z95395; E316097; -- HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-972H-;
WOOD V:, BARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (MAY-1997)
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01-JUL-1997
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                   01-JAN-1998
01-JAN-1998
01-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   BACILLUS STEAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PMK2PPA
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                                                           023979
023979;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
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                                                                                                                                                                             116
                                                                                                                                                                                                                                                                                                                                                                                                                       ROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
                                                                                                                            176 KRLKPGYLEATVDWFRRYKVPDGK
                                                                                                                                                                                                  56 DGDPLDILVITINPTFPGCVIDTRVIGYLNMYDSGEEDAKLIGVPVEDP---RFDEVRSI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFRVYCYKNNK-P-ISFFHDVPLTSDKDTFNMVTEIPRWTQAKCEISLTSPFHPIKQDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVTKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKQVKVLGALGLIDQGETDWKILAIDINDPRAKLLNDISDVQNLMPRLLPCTRDWFAIYK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGKLRYVANLEPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDNDPIDVCEIGSKVCARGE
                                                                                                                                                 EDLPQHKLKEIAHFFERYKDLQGK 136
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                                                                                                                                                                                                                                 Similarity 28; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TREMBLREL 04, TREMBLREL 04, (TREMBLREL 04,
                   8 (TREMBLREL.
3 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                        FIRMICUTES;
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                                                                                                                                                                                                                                                                                                                                                                                  12016;
                                                                                                                                                                                                                                 Conservative
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                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32898 MW;
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                                                                                                                                                                                                                                                33.3%;
                                                                                                                                                                                                                                                                                                                                                                   KOYAMA M.,
                                                                                                                                                                                                                                                                                                                                           TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                            7.2%;
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                      05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 864; DB 1; Leux
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; CREATED)
;, LAST SEQUENCE UPDATE)
5; LAST ANNOTATION UPDATE)
7 TANTASE (EC 3.6.1.1).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                    Score 154; DB 9;
Pred. No. 8.78e-10;
18; Mismatches 35
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                                                                                                                              199
                                                                                                                                                                                                                                                                                                                                                                       SAKURAI N.,
                                                                                                                                                                                                                                                                                       BD71D735 CRC32;
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Best Local S
Matches 2
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Best Local
Q49071
Q49071;
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01-JAN-1998
01-JAN-1998
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HYDROLASE.
                                                                                                                                                                                                                                 SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AE000812; G2621313; -. SEQUENCE 176 AA; 20084 MW; 66900C6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                   SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DU ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K., HARRISON D., HOANG L., KEACLE P., LUMM W., POTHIER B., QIU D. SPADAFORA R., WICARE R., WANG Y., WIERZBOWSKI J., GIBSON R., SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VISSER K., HEIMOVAARA-DIJKSTRA S., KIJNE ;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ
EMBL, AF009675; G2258074; -.
                                                                                                                                                                                                                                                                          SMITH D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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SEED PLANTS; MAGNOLIOPHYTA;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.; J. BACTERIOL. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-DELTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHANOBACTERIUM THERMOAUTOTROPHICUM
ARCHAEBACTERIA; EURYARCHAEOTA; METHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   026363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HORDEUM VULGARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HORDEUM VULGARE VAR. DISTICHUM (TWO-ROWED BARLEY)
EUKARYOTAE; MITOCHONDRIAL EUKARYOTES; VIRIDIPLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHANOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 CEDNDPMDVLVLMQEPVIPGSFLRARAIGLMPMIDQGEKDDKIIAVCADDPEYRHYSTSV 160
                                                                                                                          116
                                                                                                126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 NDVKRL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 SLLPRL 166
                                                                     176 KRLKPGYLEATVDWFRRYKVPDGK 199
                                                                                                                                                                                                                                                                                                                                                                          IWANI N., CARUSO A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26363;
                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYN-DI 172
                                                                                             -P-EHN-LKEIANFFETYKKLEGK 146
                                                                                                                        DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV 175
                                                                                                                                               DGDPMDILVLMDEPTFPGCIIESRPIGLLRMIDGGDQDDKILAVPVADPHFADVKDISDI 125
                                                                                                                                                                            Similarity 34.5%
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYROPHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TREMBLREL.)
(TREMBLREL.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
              PRELIMINARY;
                                                                                                                                                                                        34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.78;
36.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24049 MW;
                                                                                                                                                                                                                                                                                                                                                                          BUSH D., SAFER H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05,05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCHUM (TWO NOTHER EUKARYOTES; VIRIDIPLANTAE;

EUKARYOTES; VIRIDIPLANTAE;

OUP; EMBRYOPHYTA; VASCULAR PLANTS;

OUP; EMBRYOPHYTA; POACEAE; HORDEUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                           Score 135; DB 9; I
Pred. No. 1.50e-06;
16; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 143; DB 8; L
Pred. No. 6.87e-08;
18; Mismatches 23;
              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHANOBACTERIALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DF89ED71
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              136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC32;
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                                                                                                                                                                                                                                                                                                                                                                       PATWELL D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UPDATE)
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BANKS.
                                                                                                                                                                                                Length 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 215
                                                                                                                                                                                                                                                                                                                                                             CHURCH G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                     Ū.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 DUBOIS
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RESULT
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Best Local
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Best Local
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034955,

01-JAN-1998 (TREMBLREL. 0

01-JAN-1998 (TREMBLREL. 0

01-JAN-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           022537
                                                                                                                                                                                                                                                                                               STRAIN-MILYANG 23; TISSUE-SEED;
LEE M.C., KIM C.S., EUN M.Y.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF022733; G2570501; -..
                                                                                                                                                                                                                                                                                                                                                                                 ORYZA SATIVA (RICE).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 27343(KID);
MEDLINE; 96059641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
                                                                                                                                                                                                                                                                                        SEQUENCE
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                                   INORGANIC
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            CYPERALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30RK P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROKARYOTA; TENERICUTES; MOLLICUTES; MYCOPLASMA;
                                                                                                                                            174
                                                                                                                                                                   157
                                                                                                                                                                                          114
                                                                                                                                                                                                                                                                                                                                                                                                                           NORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYCOPLASMATACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORK P., OUZOUNIS C., CASARI G., ILLBERT W., GILLEVET P.M.;
DL. MICROBIOL. 16:955-967(1995)
MBL; Z33286; G530477; ...
DN_TER. 1.1.
                                                                                                                                                                                                                 98
                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                          DVKRLKPGYLEATVDWFRRYKVPDGKP-E-NEFAFNAE
                                                                                                                                                                                                               CEDGDPMDVLVLMQEQVVPGCFLRARAIGLMPMIDQGEKDDKIIAVRADDLNTAT-SGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -P-KH-YRXXXXXFFLQYKALQNK
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                                                                                                                                                      RKSPFTA-FKRSAV-FFEDYKKNENKEVAVNEF-FPAE:::::| | | | | | | | | | | | | |
                                                                                                                                                                                         CGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                 998 (TREMBLREL. 05,
998 (TREMBLREL. 05,
998 (TREMBLREL. 05,
998 (TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                           PYROPHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYROPHOSPHATASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                            GRAMINEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 AA;
                                                                                                                                                                                                                                                                                        214 AA;
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 126; DB 9; 31.0%; Pred. No. 4.35e-05;
                                                                                                                                                                                                                                                 31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15815 MW;
                                                                                                                                                                                                                                                                                        23610 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                      Pred.
22; 1
                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                  Score 123; DB 8; Pred. No. 1.30e-04
                                                                                                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                             PRT;
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                                                                                                                                                                                                                                                                                       ED159571 CRC32;
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                                                                                                                                                                                                                                       Mismatches
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                                                                                               178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
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                                                                                                                                                                 191
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                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                              BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SANDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYCOPLASMATALES;
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PPA.
LEGIONELLA PNEUMOPHILA
PROKARYOTA; GRACILICUTI

GRACILICUTES;

SCOTOBACTERIA; AEROBIC RODS AND COCCI;

EGIONELLACEAE

EQUENCE FROM N.A

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Best Local
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EMBL; AF031464; G2642277; -
EMBL; AF030232; G2613038; -
EMBL; AF030232; G2613038; -
SEQUENCE 178 AA; 20049 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-AA10
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01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
MHC CLASS I ATBE-G*03 (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATBE-G.
ATELES BELZEBUTH (LONG-HAIRED
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 KRLKPGYLEATVD-WFRRYK-VPDGK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
CADAVID L.F., SHUFFLEBOTHAM C.,
WATKINS D.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U59650; G1389913: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KWAIK
                                                                                                                                                                                                                                        Q41676;
                                                                                                                                                                                                                                                                                                                                                                            141 VLNEDLRSWTAADLAAQITQR-KWEAANAAERMRA-YLEGTCYEWLRRY-LENGK 192 ::: | |::: |||:| :::|| :::|
SEQUENCE FROM N.A.
TISSUE-COTYLEDON;
NONG V., BECKER C.
                                                                                                                              VICIA NARBONENSIS
                                                                                                                                                                              01-JAN-1998
                                                                                                                                                                                                                01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                 146 MIDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEAT-VDWFRRYKVPDGK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KWAIK Y:;
                                                                                                              EUKARYOTA; PLANTAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDI-PQHLLLSIEHFFKHYKDLEEGK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUN. 66:0-0(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .ps00290;
                                                                                           FABALES; FABACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.
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                                                                                                                                                                          6 (TREMBLREL.
6 (TREMBLREL.
8 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                               5.1%;
larity 27.3%;
Conservative
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                                                                                                                                                                                                                                                                  PRELIMINARY;
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27.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40827
                                                                                                                  EMBRYOBIONTA;
         MUENTZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91,01
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21; 1
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108; DB 5;
Pred. No. 2.50e-02;
16; Mismatches 20
                                                                                                                                                                                   CREATED)
LAST SEQUENCE ANNUAL AST ANNUAL ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPIDER MONKEY)
VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E3505B05 CRC32;
                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0E4A568E CRC32;
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No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RUIZ F.J.,
                                                                                                                                                                                      SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                       MAGNOLIOPHYTA; MAGNOLIOPSIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
1.12e-03;
1.3s 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363
                                                                                                                                                                                                                                                                              482
                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUGHES
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                            Q30444;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                030444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
                                                                                                                                                                                                                                                                                                     CADAVID L.F.,
WATKINS D.I.;
SUBMITTED (JUN
                                                                                                                                                                                                                                                                                                                                                       CALLITHRIX JACCHUS (
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 RY-KVPDGKPENEFAFNAEFKD-K-DFAIDIIK
                                                                                                                                                                                                                                                                                                                                                                                     MHC CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 RYQREQGGKQEQENDGNNIFSGFKRDFLEDALN
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                           EMBL; U59640;
                                                                                                                                                                                                                                                                                                                                                 THERIA;
                                                                                                               01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                           NON_TER
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                                                                                                PAN TROGLODYTES (CHIMPANZEE)
                                                                                                                                                                                         147 IDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEAT-VDWFRRYKVPDGK 199
                                                                                                                                                                                                  142 LNEDLRSWTAPDVAAQITQR-KWEAANEAER-RRAYLEGTCVEWLRRY-LENGK
                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE BOND SIMILARITY: TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT:
 EMBL; U1(
PROSITE;
MHC.
                        MCADAM S.N., BOYSON J.E.,
BONTROP R.E., WATKINS D.I
BONTROP R.E., WATKINS D.I
J. IMMUNOL. 154:6421-6429
                                                   SEQUENCE FROM N.A. MEDLINE, 95279794.
                                                                               EUTHERIA;
                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEIIGVKYLGILAMIDEGETDWKYIAINVDDPDAANYNDINDVKRLKPGYLEATVDW-FR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDIIAVPTGNVLWMYNDODTP--VIAISLTDTGSSN-NOLDQIPR-R-FYLAGNOEQEFL 192
                  IMMUNOL. 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00305;
                                                                                                                                                                                                                             Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                  PRIMATES
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                                                                                                                                                                                                                                                                                                     (JUN-1996)
                                                                                                                                                                                                                                                                                                                                                                                            6 (TREMBLREL.
5 (TREMBLREL.
5 (TREMBLREL.
                                                                               PRIMATES.
                                                                                                                                                                                                                                                                   356 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEXAMER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                             5.0%;
llarity 27.8%;
Conservative
                                                                                        METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                             JN-1996) TO 1; G1389927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                       SHUFFLEBOTHAM C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                    AA;
                                                                                                           (FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11S_SEED_STORAGE; 1.
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
OTHER 11S SEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54667 MW;
                                                                                                                                                                                                                                                                                                                                                            (COMMON MARMOSET).
CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO EMBL/GENBANK/DDBJ DATA BANKS.
EACH SUBUNIT IS COMPOSED OF AN
ED FROM A SINGLE PRECURSOR AND I
                                                                                                                                                                                                                                                                     39894
           IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                      01, CREATED)
01, LAST SEQUENCE UP
01, LAST ANNOTATION
(FRAGMENT)
                            -6429(1995).
                                                                                                                                                                                                                                                                                                       EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                              01,
                                                                                                                     05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109;
Pred. No. 1.
21; Mismatc
                                                                                                                                                                                                                                                                      WW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
901C5103
                                              LIU
                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                Score 106; DB 5;
Pred. No. 4.87e-02
15; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                           PRT;
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                                               ×:
                                                                                            VERTEBRATA;
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                                                 GARBER
                                                                                                                                                                                                                                                                                                                                                                                                                                       356 AA
                                                                                                                                                                                                                                                                                                                            F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8;
.78e-02;
                                                                                                                                                              357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEINS (GLOBULINS)
                                                                                                                                                                                                                                                                                                                                                                 TETRAPODA;
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                                                                                             TETRAPODA;
                                                                                                                                                                                                                                                                                                                             YEAGER
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                                                    HUGHES
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LINKED B
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                                                                                                                                                                                                                                                                                                                               HUGHES
                                                                                                MAMMALIA;
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BY A
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Best Local Similarity
Thes 15; Consert
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            Query Match 5.0%;
Best Local Similarity 27.0%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                019445
019445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q08680;
             LAMBRACHT D., DUEVEL SUBMITTED (NOV-1997)
                                                                                                                                                                      RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                          01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
MHC CLASS IB ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WALTER L., HEINE L., GUENTHER E.; IMMUNOGENETICS 39:351-354(1994).
EMBL; X70066; G56610; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=LEW/GUN; TISSUE=CONA STIMULATED LYMPHOCYTES;
MEDLINE; 94222444.
WALTER L., HEINE L., GUENTHER E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
SEQUENCE FROM N.A.
                                                  STRAIN-LEW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                             SEQUENCE FROM N.A.
                                                                                       MEDLINE; 95278971.
LAMBRACHT D., WONIGEIT K.;
LAMBRACHTICS 41:375-379(1995).
                                                                                                                                SEQUENCE FROM N.A.
STRAIN-LEW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 -YLOGTCVEWLRRY 192
                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASS
                                                                                                                                                                                                                                                                                                                                                GYLEAT-VDWFRRY 193
                                                                                                                                                                                                                                                                                                                                                                                                 CEIGSKVCA-RG-EIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP 180
                                                                                                                                                                                                                                                                                                                                                                                                                         CDVGSDGSLLRGYDQFAYDGRDYLALNEDLKT-WMA-ADTAAQMTRNKWDQAGEAERHKA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 AA; 41053 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TREMBLREL 01, CREATED)
(TREMBLEL 01, LAST SEQUENCE UPDATE)
(TREMBLEL 05, LAST ANNOTATION UPDATE)
HISTOCOMPATIBILITY ANTIGEN, LW2 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.0%;
larity 27.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                            PRELIMINARY;
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39890 MW;
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                        o,
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                       WONIGEIT K.;
EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 107; DB 5; L
Pred. No. 3.49e-02;
15; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 107; DB 5; Length 367
Pred. No. 3.49e-02;
19; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
RT1 CLASS I HISTOCOMPATIBILITY ANTIGEN,
LWZ ALPHA CHAIN.
60475057 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                    VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24BF11F7 CRC32;
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                                                                                                                                                                                                                                                                                            377 AA.
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Search completed: Thu Sep 17 Job time: 124 secs.
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Best Local Similarity 27.0%;
Matches 20; Conservative
                                                                                                                                                                                                    STRAIN-LEW;
LAMBRACHT D.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF025308; G2570821; -
SEQUENCE 377 AA; 42200 MW; 335C92C1 CRC32;
                                                                                                                                    122 CDVGSDGSLLRGYDQFAYDGRDYLALNEDLKT-WMA-ADTAAQMTRNKWDQAGEAERHKA 179
                                                        181 GYLEAT-VDWFRRY
                                                                                  180 -YLQGTCVEWLRRY 192
                                                                                                                123 CEIGSKVCA-RG-EIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP 180
                                                         193
               16:57:04 1998
                                                                                                                                                                       Score 107; DB 5;
Pred. No. 3.49e-02
19; Mismatches 2
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